

STIC-Biotech/ChemLib

112172

From: Ramirez, Delia
Sent: Wednesday, January 14, 2004 5:38 PM
To: STIC-Biotech/ChemLib
Subject: case 09/847081

Hi,

I would like to request the following interference searches: seq id 1 and 2 in the nucleic acid databases.

Thank you,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
1911 S. Clark Street, Crystal Mall # 10D06, Mail room 10D01
Arlington, VA 22202
(703) 306-0288
delia.ramirez@uspto.gov

RECEIVED
JAN 15 2004
(STIC)

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 1/15/04
Date Completed: 1/16/04
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH: /
NA Sequences: _____
AA Sequences: _____ - review to
Structures: _____ NA
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
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VERSION X68017.1
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Romer S., Huquaney P., Bouvier F., Camara B. and Kuntz M.
Expression of the genes encoding the early carotenoid biosynthetic
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Biochem. Biophys. Res. Commun. 196 (3), 1414-1421 (1993)
JOURNAL MEDLINE 8250898
PUBMED 2 (bases 1 to 1295)
AUTHORS Kuntz M.
TITLE Direct Submision
REFERENCE Submitted (30-JUL-1992) M. Kuntz, Inst. de Biologie Molec. des
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 AUTHORS Bird, C. Roger., Grierson, D., and Schuch, W. Walter.
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 JOURNAL Patent: US 5750865-A 2 12-MAY-1998;
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48.7%; Score 842; DB 6; Length 1646;

best local similarity 75.3%; file: NO_16-175;
Matches 1222; Conservative 0; Mismatches 330; Indels 92; Gaps 9

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DEFINITION			PLN 11-MAY-1995
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VERSION			
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ACCESSION  A68204
VERSION    A68204.1 GI:4759372
KEYWORDS   Lycopersicon esculentum (tomato)
SOURCE     Lycopersicon esculentum
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 1239)
 Drake, C.R., Bird, C.R. and Schuch, W.W.
 TITLE ENHANCEMENT OF GENE EXPRESSION
 JOURNAL Patent: WO 9746690-A 2 11-DEC-1997;
 ZENECA LTD (GB)

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 DEFINITION Sequence 2 from patent US 6239331.
 ACCESSION AR156064
 VERSION AR156064.1 GI:15124117
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 unclassified.

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 1 (bases 1 to 1239)
 Drake, C.R., Bird, C.R., and Schuch, W.W., Walter.
 TITLE Enhancement of tomato phytoene synthase gene expression with a modified DNA
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 Matches 917; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

466 GGTGGATCAAGAGTGAAGGAGCACTTCTCTGACAGTCCAGTTTGGTGGCTAGC 525
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 ACCESSION BD005486.1 GI:18633857
 VERSION JP 2001501810-A/2.
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 1 (bases 1 to 1239)
 AUTHORS Drake, C.R., Bird, C.R. and Schuch, W.W.
 TITLE Enhancement of gene expression
 JOURNAL Patent: JP 2001501810-A 2 13-FEB-2001;
 ZENECA LTD
 COMMENT OS Lycopersicon esculentum (tomato)
 PN JP 2001501810-A/2
 PD 13-FEB-2001

PF 23-MAY-1997 JP 1998500302
 PR 07-JUN-1996 GB 9611981.3
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 PC C12N15/67, C12N15/82, C12N15/29, C07K14/415
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 CC Topology: Linear;
 CC Key source
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 ACCESSION X67144.1 GI:19346
 VERSION GTOMS gene; mutant; phytoene synthase.
 KEYWORDS Lycopodium esculentum (tomato)
 SOURCE Lycopodium esculentum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 REFERENCE 1 (bases 1 to 1355)
 AUTHORS Fray, R.G. and Grierson, D.
 TITLE Identification and genetic analysis of normal and mutant phytoene synthase genes of tomato by sequencing, complementation and co-suppression
 JOURNAL Plant Mol. Biol. 22 (4), 589-602 (1993)
 MEDLINE 93344508
 PUBMED 8343597
 REFERENCE 2 (bases 1 to 1355)
 AUTHORS Fray, R.G.
 TITLE Direct Submission
 JOURNAL Submitted (01-JUL-1992) R.G. Fray, University of Nottingham, School of Agriculture, Sutton Bonington, Loughborough, Leicestershire LE12 5RD, UK
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 ACCESSION AF220218
 VERSION AF220218.1 GI:6959859
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 ORGANISM Citrus unshiu
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 REFERENCE 1 (bases 1 to 1506)
 Kim, I.-J., Ko, K.-C., Kim, C.-S. and Chung, W.-I.
 Isolation of a cDNA encoding phytoene synthase from Citrus
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 JOURNAL 2 (bases 1 to 1506)
 Kim, I.-J., Ko, K.-C., Kim, C.-S. and Chung, W.-I.
 Direct Submission
 Submitted (30-DEC-1999) Biological Sciences, Korea Advanced
 Institute of Science and Technology, 373-1 Kusong-dong, Yuseong-gu,
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LOCUS AB037975

DEFINITION Citrus unshiu mRNA for phytoene synthase, complete cds.

ACCESSION AB037975

VERSION AB037975.1 GI:11344506

KEYWORDS phytoene synthase.

SOURCE Citrus unshiu

ORGANISM Citrus unshiu

REFERENCE 1 (sites)

AUTHORS Ikoma,Y., Komatsu,A., Kita,M., Ogawa,K., Omura,M., Yano,M. and Moriguchi,T.

TITLE Expression of a phytoene synthase gene and characteristic carotenoid accumulation during citrus fruit development

JOURNAL Physiol. Plantarum 111, 232-238 (2001)

AUTHORS Moriguchi,T.

REFERENCE Direct Submission

JOURNAL Submitted (04-FEB-2000) Takaya Moriguchi, National Institute of Fruit Tree Science, Department of Research Planning and Coordination; 2-1 Fujimoto, Tsukuba, Ibaraki 305-8605, Japan (E-mail: takaya@fruit.affrc.go.jp, Tel:81-298-38-6416, Fax:81-298-38-6437)

FEATURES

source Location/Qualifiers

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BASE COUNT 512 a 302 c 388 g 487 t

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Query Match 40.3%; Score 696.8; DB 8; Length 1689;

Best Local Similarity 71.2%; Pred. No. 2.1e-159;

Matches 949; Conservative 0; Mismatches 377; Indels 6; Gaps 2;

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ACCESSION      E15683
VERSION      E15683.1 GI:5710366
KEYWORDS      JP 1998084966-A/4.
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE      1 (bases 1 to 2868)
AUTHORS      Koizumi, H., Kobayashi, H. and Yamamura, S.
TITLE      NEW PHYTOENE SYNTHASE GENE
JOURNAL      Patent: JP 1998084966-A 4 07-APR-1998;
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location/Qualifiers
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QY      837 AACTCCGACCTTTAGATAGTGGAGACAGGCTGGAAGATATTTCACTGAGCGGCC 896
Db      966 AATCCCAACCGCTTAGATAGTGGAGACAGATAGAGATGTTTCAAGGCGCAAC 1025
QY      897 ATTGATATGCTGATGCTGCTTTATCCGATAGCTGTCCAGATTTCTGTTGATATCA 956
Db      1026 TTTGATATGCTTATGATGCTGCTTTATCTGATACCATTCACAGATCTCTGAGCATCA 1085
QY      957 GCCATTCAGATATGATTAAGAGATGCTATGAGCTTGTGAAATCAGATACAAAC 1016
Db      1086 GCCATTTAGATATGATTAAGAGATGCTATGAGCTTGTGAAATCAGATACAAAC 1145
QY      1017 TTTGATAGCTATATCTCTATTTGTTACTATGTTGCTGTGCTGTGATGATGATGCT 1076
Db      1146 TTTGATAGCTATATCTCTATTTGTTACTATGTTGCTGTGCTGTGATGATGATGCT 1205
QY      1077 TCCAGTTATGAGTATGTCACCTGATCAAGAGCAACAGAGAGTGTATTAATGCTGC 1136
Db      1206 ACCAGTATGAGGATGACCTGATCTGATCTGAGGCAACAGAAAGTGTATTAATGCTGC 1265
QY      1137 TTTGCTTTAGGCTTGGCAATCACTAACCAATATATCTAGAGATGTAAGAGATGC 1196
Db      1266 TTTATCTTTGGGATGCGGACCAAGCTGATCAATCTTAAGGATGTTGAGAAAGATGC 1325
QY      1197 CAGAGAGAGAGATATCTTCTGCTCAAGATGATTAAGACAGGAGGCTCTCGACGA 1256
Db      1326 AAGAGAGAGAGATGATCTTCACTCAAGATGATTAAGACAGGAGGCTTATCAGATGA 1385
QY      1257 AGACATATTTGCTGGAAGATGATGATGATGAGAGAACTTTTGAAGAAACAAATCA 1316
Db      1386 GACATTTTCTGGAAGATGATGATGATGAGAGAACTTTTGAAGAAACAAATCA 1445
QY      1317 GAGGCGAGAGAAATCTTGTATGATGATGAGAGAAAGTGTCAAGAACTGACTGCTGC-TA 1375
Db      1446 AAGGCTTGAAGAAATCTTGTATGATGATGAGAGAAAGTGTCCCGAAGCTCAGCTCGGAA 1505
QY      1376 GTAGATGCTGTGTAAAC--AGGCTGCTGTTGATGCAAGATATGAGACGATGTA 1433
Db      1506 GCAGATTTCTGCTGTGAGGCGCAGGCTTCTTTTATGAAAAAATATGATGATGATGTA 1565
QY      1434 AGGCAAGATCAACAACATTCACAGAGAGGCTTATGTTAGCAAGCCAAAGAGCTTCT 1493
Db      1566 AGCAATAGCTACACAAATTTCAACAAGAGGCTTATGTTAACAAGGCAAGAGCTATTT 1625
QY      1494 CACCTTGCCATGCTTATGCAAAATCTCT 1523
Db      1626 AGCTATGCTGATGATGCAAGTCTCT 1655

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Search completed: January 16, 2004, 03:01:50
Job time : 6329 secs

XX WPI: 2002-02736/04.
 DR P-PSDB; AAM51841.
 XX
 PT New nucleic acid encoding tobacco zeta-carotene desaturase, useful for
 screening compounds with herbicidal activity -
 PS
 XX Claim 14; Page 12-17; 44pp; German.
 CC The present invention provides the protein and coding sequences of
 CC phytoene synthase and zeta-carotene desaturase from *Nicotiana tabacum*.
 CC The sequences can be used to identify compounds capable of altering the
 CC expression of these genes, which are therefore useful as plant growth
 CC regulators and herbicides. They can also be used to produce transgenic
 CC plants. The present sequence is the coding sequence of a tobacco
 CC phytoene synthase.
 CC
 XX Sequence 1728 BP; 513 A; 290 C; 433 G; 492 T; 0 other;
 SO
 Query Match 100.0%; Score 1728; DB 24; Length 1728;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAACCCAGAAAGAACCAAGCTTTGCTTGTGATGAGTGCATTGCTTGTCTT
 DB 1 AGAAACCCAGAAAGAACCAAGCTTTGCTTGTGATGAGTGCATTGCTTGTCTT
 QY 61 GTGTAGGCAAGAGTGGTTCCTTCTTATCCGATTTTATCGTTGAAATTAATG
 DB 61 GTGTAGGCAAGAGTGGTTCCTTCTTATCCGATTTTATCGTTGAAATTAATG
 QY 121 GATAGACTCTAGTGTATCTACAGTATGTTGTTTGTATGATTAAGCTGAGTGA
 DB 121 GATAGACTCTAGTGTATCTACAGTATGTTGTTTGTATGATTAAGCTGAGTGA
 QY 121 GATAGACTCTAGTGTATCTACAGTATGTTGTTTGTATGATTAAGCTGAGTGA
 DB 121 GATAGACTCTAGTGTATCTACAGTATGTTGTTTGTATGATTAAGCTGAGTGA
 QY 181 AGTAACTAAGAAAGAACCAAACTTGGGAATTTTGAACCAAGGTTTCTTGT
 DB 181 AGTAACTAAGAAAGAACCAAACTTGGGAATTTTGAACCAAGGTTTCTTGT
 QY 181 AGTAACTAAGAAAGAACCAAACTTGGGAATTTTGAACCAAGGTTTCTTGT
 DB 181 AGTAACTAAGAAAGAACCAAACTTGGGAATTTTGAACCAAGGTTTCTTGT
 QY 241 TTCAAGACATGCTGTTGCTTGTGTTGTTGTTTCTCCACATCCGAGTCCGAT
 DB 241 TTCAAGACATGCTGTTGCTTGTGTTGTTGTTTCTCCACATCCGAGTCCGAT
 QY 241 TTCAAGACATGCTGTTGCTTGTGTTGTTGTTTCTCCACATCCGAGTCCGAT
 DB 241 TTCAAGACATGCTGTTGCTTGTGTTGTTGTTTCTCCACATCCGAGTCCGAT
 QY 301 GGGACAGATGTTGATTCAGTCCGAGAAAGAACCCGCTTGTATCAACAGTTC
 DB 301 GGGACAGATGTTGATTCAGTCCGAGAAAGAACCCGCTTGTATCAACAGTTC
 QY 301 GGGACAGATGTTGATTCAGTCCGAGAAAGAACCCGCTTGTATCAACAGTTC
 DB 301 GGGACAGATGTTGATTCAGTCCGAGAAAGAACCCGCTTGTATCAACAGTTC
 QY 361 CTAGCTCGAGATGAGAAATTTGATGGAATGGGAATCAAGAAAGTGGGAGCAAAAG
 DB 361 CTAGCTCGAGATGAGAAATTTGATGGAATGGGAATCAAGAAAGTGGGAGCAAAAG
 QY 361 CTAGCTCGAGATGAGAAATTTGATGGAATGGGAATCAAGAAAGTGGGAGCAAAAG
 DB 361 CTAGCTCGAGATGAGAAATTTGATGGAATGGGAATCAAGAAAGTGGGAGCAAAAG
 QY 421 TGGAAATTTGCTCTTAATTTGCTGATCCAGATATTCATGTTGGTGAATCAAGAACT
 DB 421 TGGAAATTTGCTCTTAATTTGCTGATCCAGATATTCATGTTGGTGAATCAAGAACT
 QY 421 TGGAAATTTGCTCTTAATTTGCTGATCCAGATATTCATGTTGGTGAATCAAGAACT
 DB 421 TGGAAATTTGCTCTTAATTTGCTGATCCAGATATTCATGTTGGTGAATCAAGAACT
 QY 481 GAAAAGGAGAGCACTTCTCTGTACAGTCCAGTGTGCTGAGCCGAGCTGAGAAATG
 DB 481 GAAAAGGAGAGCACTTCTCTGTACAGTCCAGTGTGCTGAGCCGAGCTGAGAAATG
 QY 481 GAAAAGGAGAGCACTTCTCTGTACAGTCCAGTGTGCTGAGCCGAGCTGAGAAATG
 DB 481 GAAAAGGAGAGCACTTCTCTGTACAGTCCAGTGTGCTGAGCCGAGCTGAGAAATG
 QY 541 ACTGTGTATCAGAGAAAGGTGTATGATGTATTAAGCAGGAGCTTTAGTGAAG
 DB 541 ACTGTGTATCAGAGAAAGGTGTATGATGTATTAAGCAGGAGCTTTAGTGAAG
 QY 541 ACTGTGTATCAGAGAAAGGTGTATGATGTATTAAGCAGGAGCTTTAGTGAAG
 DB 541 ACTGTGTATCAGAGAAAGGTGTATGATGTATTAAGCAGGAGCTTTAGTGAAG
 QY 601 AGGACGCTGAGATCTACCGATGATTTAGAGTGAAGCCGAGATATTGTTCCAGGGAT
 DB 601 AGGACGCTGAGATCTACCGATGATTTAGAGTGAAGCCGAGATATTGTTCCAGGGAT
 QY 601 AGGACGCTGAGATCTACCGATGATTTAGAGTGAAGCCGAGATATTGTTCCAGGGAT
 DB 601 AGGACGCTGAGATCTACCGATGATTTAGAGTGAAGCCGAGATATTGTTCCAGGGAT
 QY 661 TTGGCTTGTGAGTGAAGCATATGATGTTGGCGAAGTATGTCAGAGTATCAAG
 DB 661 TTGGCTTGTGAGTGAAGCATATGATGTTGGCGAAGTATGTCAGAGTATCAAG
 QY 661 TTGGCTTGTGAGTGAAGCATATGATGTTGGCGAAGTATGTCAGAGTATCAAG
 DB 661 TTGGCTTGTGAGTGAAGCATATGATGTTGGCGAAGTATGTCAGAGTATCAAG
 QY 721 ACATTTTACTTGAAGCAAGCTAATGACCCAGAGAGAGAGAGCTATCTGGGCAATA
 DB 721 ACATTTTACTTGAAGCAAGCTAATGACCCAGAGAGAGAGAGCTATCTGGGCAATA

DB 721 ACATTTTACTTGAAGCAAGCTAATGACCCAGAGAGAGAGAGCTATCTGGGCAATA
 QY 781 TATGTGTGAG
 DB 781 TATGTGTGAG
 QY 841 CCGCAAGCTTTAGTATGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 DB 841 CCGCAAGCTTTAGTATGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 QY 901 GATATGCTTGTATGCTCTTATTCGATACCTGCTCCAGATTTCTGTTGATATTCAGCA
 DB 901 GATATGCTTGTATGCTCTTATTCGATACCTGCTCCAGATTTCTGTTGATATTCAGCA
 QY 901 GATATGCTTGTATGCTCTTATTCGATACCTGCTCCAGATTTCTGTTGATATTCAGCA
 DB 901 GATATGCTTGTATGCTCTTATTCGATACCTGCTCCAGATTTCTGTTGATATTCAGCA
 QY 961 TTGAGATATGATTTGAAG
 DB 961 TTGAGATATGATTTGAAG
 QY 961 TTGAGATATGATTTGAAG
 DB 961 TTGAGATATGATTTGAAG
 QY 1021 GATAGCTATATCTTATTTGATGATGTTGCTGTAATGAGATGATGAGTTCCTCA
 DB 1021 GATAGCTATATCTTATTTGATGATGTTGCTGTAATGAGATGATGAGTTCCTCA
 QY 1021 GATAGCTATATCTTATTTGATGATGTTGCTGTAATGAGATGATGAGTTCCTCA
 DB 1021 GATAGCTATATCTTATTTGATGATGTTGCTGTAATGAGATGATGAGTTCCTCA
 QY 1081 GTTATGGGATTTGCACTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 DB 1081 GTTATGGGATTTGCACTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 QY 1081 GTTATGGGATTTGCACTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 DB 1081 GTTATGGGATTTGCACTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 QY 1141 GCTTATGGGCTTGAAGATCACTAAGATATCTGAGAGTGTAGAGAGAGAGAGAGAGAG
 DB 1141 GCTTATGGGCTTGAAGATCACTAAGATATCTGAGAGTGTAGAGAGAGAGAGAGAGAG
 QY 1201 AGAGAGAGATATCTTCTCAAGATATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 DB 1201 AGAGAGAGATATCTTCTCAAGATATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 QY 1201 AGAGAGAGATATCTTCTCAAGATATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 DB 1201 AGAGAGAGATATCTTCTCAAGATATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 QY 1261 ATATTTGCTGAG
 DB 1261 ATATTTGCTGAG
 QY 1261 ATATTTGCTGAG
 DB 1261 ATATTTGCTGAG
 QY 1321 GCGAGAGAAATCTTGTATGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 DB 1321 GCGAGAGAAATCTTGTATGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 QY 1321 GCGAGAGAAATCTTGTATGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 DB 1321 GCGAGAGAAATCTTGTATGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
 QY 1381 TGGCTGTGTTAAG
 DB 1381 TGGCTGTGTTAAG
 QY 1381 TGGCTGTGTTAAG
 DB 1381 TGGCTGTGTTAAG
 QY 1441 GACTACAACTTCAAG
 DB 1441 GACTACAACTTCAAG
 QY 1441 GACTACAACTTCAAG
 DB 1441 GACTACAACTTCAAG
 QY 1501 CCGATGCTTATGCAAAATCTTGTGAGCCCTTAATGAACTTCTCCACTGAGCAAG
 DB 1501 CCGATGCTTATGCAAAATCTTGTGAGCCCTTAATGAACTTCTCCACTGAGCAAG
 QY 1501 CCGATGCTTATGCAAAATCTTGTGAGCCCTTAATGAACTTCTCCACTGAGCAAG
 DB 1501 CCGATGCTTATGCAAAATCTTGTGAGCCCTTAATGAACTTCTCCACTGAGCAAG
 QY 1561 ACATGATGAG
 DB 1561 ACATGATGAG
 QY 1561 ACATGATGAG
 DB 1561 ACATGATGAG
 QY 1621 AATGAGATATCTTGTCTAAATGATGTATCAATCAAAAGTATGTAATTAATCAATATGACA
 DB 1621 AATGAGATATCTTGTCTAAATGATGTATCAATCAAAAGTATGTAATTAATCAATATGACA
 QY 1621 AATGAGATATCTTGTCTAAATGATGTATCAATCAAAAGTATGTAATTAATCAATATGACA
 DB 1621 AATGAGATATCTTGTCTAAATGATGTATCAATCAAAAGTATGTAATTAATCAATATGACA
 QY 1681 ATCTCTGTGAGAAATATTTCTCCACACTATCAAACTTCAAGTGAAG 1728
 DB 1681 ATCTCTGTGAGAAATATTTCTCCACACTATCAAACTTCAAGTGAAG 1728

RESULT 2

ABX13568
 ID ABX13568 standard; DNA, 1573 BP.

XX ABX13568;
 XX

DT 12-JUN-2003 (first entry)
 XX Tobacco phytoene synthase DNA.
 XX
 XX Zeaxanthin epoxidase; zeaxanthin; carotenoid; inhibitor;
 KM transgenic plant cell; alpha-tocopherol; food supplementation;
 KM tobacco; phytoene synthase; Pys; ds.
 XX
 OS Nicotiana tabacum.
 XX
 XX MO2002103021-A2.
 XX
 XX 27-DEC-2002.
 XX
 XX 19-JUN-2002; 2002WO-EP06810.
 XX
 XX 19-JUN-2001; 2001EP-0114661.
 XX
 XX (VKAM/) VON KAMEKE K.
 XX
 XX Sandmann G, Roemer S, Luebeck J, Adomat C, Kauder F;
 XX
 XX WPI; 2003-167525/16.
 XX
 XX Increasing zeaxanthin and total carotenoid contents of plants, useful
 PT for food supplementation, by inhibiting activity of zeaxanthin
 PT epoxidase -
 XX
 PS Examples; Page 34-35; 52pp; German.
 XX
 CC This invention describes a novel method of increasing the zeaxanthin
 CC and/or total carotenoid contents in transgenic plant cells, plants or
 CC other host cells or organisms (e.g. algae) by inhibiting the endogenous
 CC zeaxanthin epoxidase (ZEP) activity. The invention also discloses
 CC transgenic plant cells or plants, their harvested products, replicative
 CC material (protoplasts, calli, seeds, tubers and cuttings) and
 CC desiccants, produced by the novel method. The method is used to increase
 CC production of zeaxanthin and total carotenoids (including the therapeutic
 CC antioxidant alpha-tocopherol) for food supplementation. This sequence
 CC represents a polynucleotide corresponding to the tobacco (Nicotiana
 CC tabacum) phytoene synthase (Pys) gene which is used to describe the
 CC method of the invention.
 CC
 CC Sequence 1573 BP; 475 A; 270 C; 390 G; 432 T; 6 other;
 SQ
 Query Match 81.3%; Score 1405.6; DB 25; Length 1573;
 Best Local Similarity 97.9%; Pred. No. 0;
 Matches 1463; Conservative 0; Mismatches 25; Indels 6; Gaps 4;

QY 596 TGAAGAGCAGCTGAGATCTACCGATGTTAGAGTGAAGCCGATATTTGTTCCAG 655
 |||
 DB 365 TGAAGAGCAGCTGAGATCTACCGATGTTAGAGTGAAGCCGATATTTGTTCCAG 424
 QY 656 GGAATTTGGGCTTTGAGTGAAGATATGATCGTTGGCGAGTATGTGCAAGTATG 715
 |||
 DB 425 GGAATTTGGGCTTTGAGTGAAGATATGATCGTTGGCGAGTATGTGCAAGTATG 484
 QY 716 CAAAGACATTTTACTAGGAACCAAGCTAATGACCCGAGAGAGAAAGAGTATCTGGG 775
 |||
 DB 485 CAAAGACATTTTACTAGGAACCAAGCTAATGACCCGAGAGAGAAAGAGTATCTGGG 544
 QY 776 CAATATATGTGTGTGAGAGAAAGAGATGAGCTTTGATGAGCCCTAATGATCCACA 835
 |||
 DB 545 CAATATATGTGTGTGAGAGAAAGAGATGAGCTTTGATGAGCCCTAATGATCCACA 604
 QY 836 TAACTCCGAAGCTTTAGATAGTGGAGACAGGCTGGAAGATATTTCACTGGGCGG 895
 |||
 DB 605 TAACTCCGAAGCTTTAGATAGTGGAGACAGGCTGGAAGATATTTCACTGGGCGG 663
 QY 896 CATTTGATATGTGTGATGCTGCTTATCCGATCTGTCTCCAGATTTCTGTGATATTC 955
 |||
 DB 664 CATTTGATATGTGTGATGCTGCTTATCCGATCTGTCTCCAGATTTCTGTGATATTC 723
 QY 956 AGCCATTCAGAGATATGATTTGAAGAGATGCGATGAGCTTTGGAATTCAGATCAAAA 1015
 |||
 DB 724 AGCCATTCAGAGATATGATTTGAAGAGATGCGATGAGCTTTGGAATTCAGATCAAAA 783
 QY 1016 CTTTGATGAGCTATATCTATTTGTTACTATGTTGCTGTGATCTGTAGAGATTTGAGTG 1075
 |||
 DB 784 CTTTGATGAGCTATATCTATTTGTTACTATGTTGCTGTGATCTGTAGAGATTTGAGTG 843
 QY 1076 TTCGATATGAGTATGCTATGCACTGAAATGAAGCAACAAGAGTATATATGCTG 1135
 |||
 DB 844 TTCGATATGAGTATGCTATGCACTGAAATGAAGCAACAAGAGTATATATGCTG 903
 QY 1136 CTTTGGCTTTAGGGCTTCAATCACTAATCACTAATCACTAATCACTAATCACTAATCACT 1195
 |||
 DB 904 CTTTGGCTTTAGGGCTTCAATCACTAATCACTAATCACTAATCACTAATCACTAATCACT 963
 QY 1196 CCAGAGAGAGAAAGATATCTTCTCAAGATGAATTAAGCAGAGGCTCTCCAGC 1255
 |||
 DB 964 CCAGAGAGAGAAAGATATCTTCTCAAGATGAATTAAGCAGAGGCTCTCCAGC 1023
 QY 1256 AAGACATATTTGCTGAGAGAGTATGATTAAGTGAAGCACTTTATGAAGAAACAATTC 1315
 |||
 DB 1024 AAGACATATTTGCTGAGAGAGTATGATTAAGTGAAGCACTTTATGAAGAAACAATTC 1083
 QY 1316 AGAGGCGAGAGAAATTTCTTGATGAGTGAAGAAAGTGTACAGAACTGGACTGTGCTA 1375
 |||
 DB 1084 AGAGGCGAGAGAAATTTCTTGATGAGTGAAGAAAGTGTGTACAGAACTGGACTGTGCTA 1143
 QY 1376 GTAGATGAGCTGTGTATTAAGAGGCTGCTGTGTATGCAAGATATTTGAGCGAGTTGAAG 1435
 |||
 DB 1144 GTAGATGAGCTGTGTATTAAGAGGCTGCTGTGTATGCAAGATATTTGAGCGAGTTGAAG 1203
 QY 1436 CCAAGGATCAACAACCTTCAACAAGAGGCTTATGTTAGCAAGCCAAAGAAAGCTTCTCA 1495
 |||
 DB 1204 CCAAGGATCAACAACCTTCAACAAGAGGCTTATGTTAGCAAGCCAAAGAAAGCTTCTCA 1263
 QY 1496 CTTTGGCCCATGTC-TTATGCAAAAATCTCTGTGGCCCTAATGAACTTCCCTCCACTA 1554
 |||
 DB 1264 CTTTGGCCCATGTC-TTATGCAAAAATCTCTGTGGCCCTAATGAACTTCCCTCCACTA 1323
 QY 1555 GCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1614
 |||
 DB 1324 GCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383
 QY 1615 CTTTGAATGAGATATCTTTTGTCTAATATGTATATCAAAAGTATGTTTAAATTCAT 1674
 |||
 DB 1384 CTTTGAATGAGATATCTTTTGTCTAATATGTATATCAAAAGTATGTTTAAATTCAT 1443
 QY 1675 ATGACAAATCTCTGTGATGATATTTTCTCAACATCATCAAACTCTCAAGTGAAG 1728

QY	1151	TTGCAAAATCACTAAACAATATPACTCAGAGATGTAGAGGAAGATGCCGAAGAGAGAG	1210
Db	1185	TAGCAAAATCAACTAAACAACATCTCAGAGATGTCCGGAAGAGATGCCGAAGAGAGAG	1244
QY	1211	TATACTTCCCTCAAGATGAATTTAGCACAGGAGGGCTCTCCGACGAACATATTTTGGT	1270
Db	1245	TCTACTTACCTCAAGATGAATTTAGCACATGCAAGGCTCTCCGACGATGACATATTCGCTG	1304
QY	1271	GAAAGATGACTGATTAAGTGGAGGAACCTTTATGAAGAAACAAATTCAGAGGCGCAGGAAT	1330
Db	1305	GAAAAATGACGATTAATATGGAGAAACCTTTATGAAGAAACAAATTCAGAGGCGCAAGAAAT	1364
QY	1331	TCTTTGATGATCAGAGAAAGGTGCACAGAACTGGACTCTGCTATGATAGGCGCTGGT	1390
Db	1365	TCTTTGATGATGAGCAGAGAGAGAGATGACACACTAGCTCAGCTATGTAATAGGCGCTGAT	1424
QY	1391	TAAACGCGCTGCTGTGTATGCGCAAGATATTGGACGAATTTGAAGCCAAAGCACTACACA	1450
Db	1425	GGGCTTCTTTCGTGTATGACCGCCAGATACTGACGAATGGAAGCCAAATGACTACACA	1484
QY	1451	ACTTCACAGAGAGGGCTTATGTATGCAAGCCAAAGAGCTTCACCTTGGCCATTGCTT	1510
Db	1485	ACTTCACAAAGAGAGCTTATGTATGAGCAATCAAGAAAGCTAATTTCTTACCTATTGGCTA	1544
QY	1511	ATGCAAAATCTCTGTGCGCCCTTAATBAACG-TCTCTCCACTGACGAAGAAGATGAATG	1568
Db	1545	ATGCAAAATCTCTGTGCGCCCTTAATBAACGCTTCTCTCTGCTTAAAGGCAATGACA	1604
QY	1570	AAGTAGTTGAGTCAATG-----AGTATTATACACTAAAGAACTCAGGATCTTG	1618
Db	1605	TCAAGTTTAAATTAAGACGAAGAAAGCAATCTCTTTAAAAAAAGAAATTTATTAACGTA	1664
QY	1619	TAAATGAGATATCTTTTGCTAAATGTATATCATCAAAAAGTAGATTGT-AAATTCATATG	1677
Db	1665	GATATGTGTATGATGATGCTCACTTGATATATCATCAAAAGTAGGTGATTAATTCATATTA	1724
QY	1678	ACAAATCTCTTGATGAATAT--TTTCTCCACACTATCAAAACCTCAAACTGA	1727
Db	1725	ACAAATCTTATGAGTGTATGATATCTTAACAATCTTAAACCTTCGAGAGGA	1775

XX MPI: 2002-027336/04.
DR P-PSDB: AAM51842.
XX
XX New nucleic acid encoding tobacco zeta-carotene desaturase, useful for
PT screening compounds with herbicidal activity -
XX
XX Claim 14; Page 21-26; 44pp; German.
XX
CC The present invention provides the protein and coding sequences of
CC phytoene synthases and zeta-carotene desaturase from *Nicotiana tabacum*.
CC The sequences can be used to identify compounds capable of altering the
CC expression of these genes, which are therefore useful as plant growth
CC regulators and herbicides. They can also be used to produce transgenic
CC plants. The present sequence is the coding sequence of a tobacco
CC phytoene synthase.
XX
SQ Sequence 1712 BP; 540 A; 265 C; 421 G; 475 T; 11 other;

Query Match: 49.6%; Score 857.8; DB 24; Length 1712;
Best Local Similarity 76.7%; Pred. No. 1.3e-234;
Matches 1206; Conservative 2; Mismatches 265; Indels 100; Gaps 9

132 GTGATATCTCAAGATATGTGTTTGTATATAAATAGGCTGAGTGTAGAGGTAACATTA 191
218 GAGTAAATTTATTTATTTTATATAATTAATTAACGAGGAGGAGGAAACAGAAACAGAA 277
192 AGGAAAGCAAAAACCTGGGAATGTTTAAACCAACGAGTTCTTGTTTCATGACAT 251
278 AGTAAAGCAAAAACCTGGGAATGTTTAAAGCCAAAGTTTCCGTTCAAA--AT 334
252 GTCGTGTCCTTGTGTTGGGTTGTTTCCCACTCCGAGGCTCGAATGGGACAGGATT 311
335 GTCGTGTCCTTGTGTTGGGTTGTTTCCCACTCCGAGGCTCGAATGGGACAGGATT 391
312 GTTGGAATTCAGTCCGAGAGGAAACCGGCTCTTGTATATTCAGAGTTCTTGTCTGAGA 371
392 CTGGAATTCAGTCCGAGAGGAAACCGGCTCTTGTATATTCAGAGTTCTTGTCTGAGA 439
372 TAGGAATTTGATGTGGAATGGGAGATCAAGAAAGGTGGAGACAAAGGTGAATTTGG 431
440 TAGGAATTTGATGTGGAATGGGAGATCAAGAAAGGTGGAGATTTGG 499
432 CTCCTTAATGCTGATCCAAATATTCATGCTTGGGTGATCAAGAAACGAAAGGAG 491
500 ----- 499
492 CACTTCTCTGTAACGTCCAGTTGGTGGCTAGCCAGCTGGAGAAAT--GACTGTGTC 548
500 -----TCTGTAAAGTCTGCTATAGTGGCTACACCGCGGGAGAAATGGCGACATGAC 553
549 ATCAGAGAAAAGGTGATGATGTGATTTAAAGCAGGCAAGCTTTAGTGAAGAGCGAGCT 608
554 ATCAGAAAGAGTGGTTATGATGTGTTTAAACAAACAGAGCTTTAGTGAAGAGCAGATT 613
609 GAGATCTACCGATGATTTAAAGATGAACCGGATATTTGTTTCCAGGGAATTTGGGCTT 668
614 GAGATCTCTGATGATTTAAAGATGAACCGGAGATTCCTCTCCCGGGAATTTAGAGCTT 673
669 GTTGAAGTAAGCATATGATGCTGTGGGGGAGAGTATGTGCAAGTAATGCAAGACATTTTA 728
674 GTTGAAGTAAGCATATGATGCTGTGGGGGAGAGTATGTGCAAGTAATGCAAGACATTTTA 733
729 CTTAGAAACCAAGCTAATGATGACCCCGAGAGAAAGAGCATATCTGGGCAATATATGTGTG 788
734 CTTAGAAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 793
789 GTGCAAGAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 848
794 GTGCAAGAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 853
849 TTTAGATAGGTGAGAGACGAGCTGGAAGATTTTCACTGGGCGGCAATTTGATATGCT 908

Db 854 CTTAGATAGGTGGGAAGACCGCTGGAAGTGTTCACGGGGGACCATTTGATATGCT 913
 QY 909 TGAATGCTTTATCCGATATCTGTCCAGATTTCCTGTGATATTCAGCCATTGAGAG 968
 Db 914 CGATGCTGCTTTGTCGGAATCTGTTCCAGTTTCCAGTTGATATTCAGCCGTTGAGAG 973
 QY 969 TATGATTTGAAGAAATCGTATGAGCTTTGTGAAATCCAGATACAAACTTTTCAGTACGT 1028
 Db 974 TATGATTTGAAGAAATCGTATGAGCTTTGTGAAATCCAGATATGAAACTTTGATGAGCT 1033
 QY 1029 AATATCTTATTTGATATGATGTTGCTGTACTGTAGATTTGATGATGTTTCCAGTTATGG 1088
 Db 1034 TTAACCTTATTTGATATGATGTTGCTGTACTGTAGATTTGATGATGTTTCCAGTTATGG 1093
 QY 1089 TATTGACCTGATCAAGGCAACACAGAGAGTGTATATATGCTGCTTTGCTTTAGG 1148
 Db 1094 TATTGACCTGATTTCAAGGCAACACAGAGAGCTATATATGACGCTTTGCTTTAGG 1153
 QY 1149 GCTTGGAAATCACTAACCAATATCTCAGAGATGTAGAGAAAGATGCCAGAAAGAAAG 1208
 Db 1154 AATCGCAATCACTAACCAATATCTCAGAGATGTAGAGAAAGATGCCAGAAAGAAAG 1213
 QY 1209 AGATATCTTGCCTCAGATGATATGACACAGAGAGGCTCTCCGACGAAAGCATATTTGC 1268
 Db 1214 AGCTTACTTACCTCAAGATGAATTTACACAGAGAGGCTCTCTGACGATGACATATTTGC 1273
 QY 1269 TGGAAAGATGACTGATATGAGAGAACTTTATGAAGAAACAAATTCAGAGGGCGAGAA 1328
 Db 1274 TGGAAAGATGACTGATATGAGAGAACTTTATGAAGAAACAAATTCAGAGGGCGAGAA 1333
 QY 1329 ATTCTTTGATGATGACAGAGAAAGTGTCAAGAACTGACTGTATGATGATGAGCTGT 1388
 Db 1334 GTTCTTCGATGAGGAGAGAGAGAGATTTACAACTGAGCTCAGTACGATGAGCTGT 1393
 QY 1389 GTTAAAGAGGCTGCTGTGTGTATGCAAGATTTGACGAGATTTGAAGCCCAAGACTTACA 1448
 Db 1394 ATGGGATCTTGTGCTGTGTGTATGACGCAAAATACGAGATTTGAAGCCCAATGACTTACA 1453
 QY 1449 CAACCTCACAAGAGAGGCTTATGTAGCAAGCCAAAGAGCTTCAACCTTGCCCATTCG 1508
 Db 1454 CAACCTCACAAGAGAGGCTTATGTAGCAAGCCAAAGAGCTTATTTCTTACTTATTCG 1513
 QY 1509 TTAATGCAAAATCTTGTGCCCCCTTATGAACT-TCTCTCCACTAGCAAGACATGAA 1567
 Db 1514 TTAATGCAAAATCTTGTGCCCCCTTCAAGAACTCTGTACCTCTAGCTAGGCAATAG 1573
 QY 1568 TGAAGTATGATGATGATGATGATTAATCACTA---AGAAATCAGTACTTGTAAAT 1623
 Db 1574 CATCAGATTTAAATTAAGCAAGAAAGCATATCTGTTAAAGAAAGAAATTTCTAAAG 1633
 QY 1624 GAGATATCTT-----TGCTAAATGTGATATCAATAAGTATGATTTG-AAAATTCATA 1675
 Db 1634 TGAATATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1693
 QY 1676 TGAATATCTTCTG 1688
 Db 1694 TAACAATCTCTAG 1706
 RESULT 6
 AA03881
 ID AA03881 standard; cDNA; 1814 BP.
 XX
 AC AA03881;
 XX
 XX 29-APR-1998 (first entry)
 DE Phycoene synthase coding sequence from N. tabacum.
 XX
 XX Phycoene synthase; transgenic plant; enhanced carotenoid synthesis;
 KW ultra violet absorber; food colour; ss.
 XX
 OS Nicotiana tabacum.

XX Key Location/Qualifiers
 FH CDS 363..1595
 FT
 FT
 XX US5705624-A.
 PN
 XX
 PD 06-JAN-1998.
 XX
 PF 27-DEC-1995; 95US-0579667.
 XX
 XX 27-DEC-1995; 95US-0579667.
 XX
 XX (DELL/) DELLA-CIOPPA G. R.
 PA (FITZ/) FITZMAURICE W P.
 PA (GRILL/) GRILL L K.
 PA (HELL/) HELLMANN G M.
 PA (KUMA/) KUMAGAI M H.
 XX
 XX Della-Cioppa GR, Fitzmaurice WP, Grill LK, Hellmann GW;
 PI Kumagai MH;
 DR WPI; 1998-086196/08.
 DR P-PSDB; AAM41060.
 XX
 PT DNA encoding tobacco phytoene synthase polypeptides - useful for
 PS producing recombinant polypeptides or transgenic plants
 XX
 XX Claim 1: Column 33-36; 25pp; English.
 XX
 CC This sequence encodes the phytoene synthetase from Nicotiana tabacum.
 CC The phytoene synthetase coding sequence represents a cDNA of the
 CC invention. The isolated nucleic acid molecules are used for producing
 CC recombinant polypeptides or transgenic plants with enhanced ability to
 CC synthesise carotenoids. Phytoene has been used as a ultra violet absorber
 CC and other carotenoids have been used as food colours, animal feeds and in
 CC the pharmaceutical and cosmetics industries.
 XX
 SO Sequence 1814 BP; 577 A; 281 C; 441 G; 515 T; 0 other;
 Query Match 49.4%; Score 853.4; DB 19; Length 1814;
 Best Local Similarity 76.5%; Pred. No. 2.5e-233;
 Matches 1223; Conservative 0; Mismatches 266; Indels 110; Gaps 10;
 QY 141 TCAAGTATGCTTTTGTGATTAATAGCTGAGGTGAGAGG-----TACCTTAAG 193
 Db 250 TAAATTTATTAATTTTATTAATTAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 309
 QY 194 GAAAGCAAAACTGGGAAATGTTTGAACCAAGAGGTTTCTGTTCAATGACATGT 253
 Db 310 TAAAGCAAAACTGGGAAATGTTTGAACCAAGAGGTTTCTGTTCAATGACATGT 366
 QY 254 CTGTGCTTTGTTGGGTTGTTTCTCCACTTCGAGAGTCTGAAATGGAAGATGT 313
 Db 367 CTGTGCTTTGTTGGGTTGTTTCTCCACTTCGAGAGTCTGAAATGGAAGATGT 423
 QY 314 TGAATTCAGTCCGAGAGAGAAACCCGCTTTGTATCATCCAGGTTTCTAGCTCAGATTA 373
 Db 424 TGAATTCAGTCCGAGAGAGAAACCCGCTTTGTATCATCCAGGTTTCTAGCTCAGATTA 471
 QY 374 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 433
 Db 472 GGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 529
 QY 434 CTTTAATGCTGATCAAGATATTCATCTGTTGGTGTGATCAAGAACTGAAAAGGAGAGCA 493
 Db 530 ----- 529
 QY 494 CTTTCTGTGATAGTCAAGTATTTGTTGCTAGCCAGCTGAGAAAT---GACTGTGATCAT 550
 Db 530 ----TTCGTGTAAGTCTGTCTATGTGTGCTACACCGCGGAGAAATGCGAGATGATCAT 585
 QY 551 CAGAGAAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 610


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QY 278 CTCCTCCAGCTTCGAAATGGACGATTTGTTGATTCAGTCCGAGAGAAACC 337
DB 292 CTC---CTGTGACGCTCAAAATGGGACAAGTTTCATGGAATCACTCGGGAGGAAACC 348
QY 338 GGGCTTTTGTATCATCCAGGTTCTTAGCTCGAGATGGAATTTGATGTGGAATGGAGAA 397
DB 349 GTTTTTTTTATTCATCGAGG-----CATAGGAATTTGGTGTCCATGTAGAGAA 396
QY 398 TCAGAAAGGTGGAGACAAGGTGGAATTTTGGCTTTAATGTGCTATCCAGATAT 457
DB 397 TCATATGAGT----- 407
QY 458 CATGCTTGGGTGATCAAGACTGAAGAGAGACAATTCTGTGACAGTCCAGTTGG 517
DB 408 -----GGTGAAGCAAACTAATATGACGGAATTTTCTGACGCTGTGCTATTT 459
QY 518 TGGCTAGCCAGCTGGAGAAATGACTGTGTCTATCAGAGAAAAAGGTGATGTGAT 577
DB 460 TGGCTACTCTCATCTGGAGAACGACGATGACATCGGAACAGATGCTATGTGAT 519
QY 578 TAAAGCAGGACCTTATGTAAGAGGACGATGATCTACCGATGTTTGAAGTGAAGC 637
DB 520 TAGGCAAGGACGCTTGTGTAAGAGGCACTGAGATCTACCAATGATTTGAAGTGAAGC 579
QY 638 CGGATATTTGTTGTTCCAGGGAATTTGGGCTTGTGAGTGAAGCAATATGATCGTTGGCG 697
DB 580 CGGATATCTATTCGCGGGAATTTGGGCTTGTGAGTGAAGCAATATGATGATGTGTG 639
QY 698 AAGTATGTGCAAGTATGCAAAACATTTTACTTGAAGAACCAAGCTAATGACCCAGAGA 757
DB 640 AAGTATGTGCAAGTATGCAAAACGTTTACTTGAAGAACCTAATGATGATCCCGAGA 699
QY 758 GAAAGAGGCTATCTGGGCAATATATGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 817
DB 700 GAAAGAGGCTATCTGGGCAATATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
QY 818 GCCCTAATGATCCCAATATCTCCGCAAGCTTTAGATGAGTGGAGACAGAGCTGGAAG 877
DB 760 GCCCAAGGCAATATATATATACCCGCGACGCTTGAATGAGTGGAGAAATAGGCTAGAA 819
QY 878 AATATTTTCAAGTGGGCGGCAATTTGATATCTGTGATGCTGCTTTATCCGATCTGTCCA 937
DB 820 AATTTTCAATGAGGCGGCAATTTGATATCTGTGATGCTGCTTTATCCGATCTGTCCA 879
QY 938 GATTTCCGTGATATTTCAAGCTTCAAGATGATGATTTGAAGAAATGCTATGAGACTTGT 997
DB 880 ACTTCCAGTTGATATTCAGCAATTCAGATGATGATTTGAAGAAATGCTATGAGACTTGA 939
QY 998 GGAATATCCAGATACAAAACCTTGCATGAGCTATATCTATTTGTTACTATTTGCTGGTA 1057
DB 940 GAAATATCCAGATACAAAACCTTGCAGCACTATACCTTATTTGTTATTTGTTGCTGGTA 999
QY 1058 CTGTAGATTTGATGAGTGTTCAGATTATGGATATGCACTGATCAATCAAGCAACAG 1117
DB 1000 CGGTGGGTTGATGAGTGTTCAGATTATGGATATGCGCCCTGATCAAGCAACAG 1059
QY 1118 AAGAGTATATATGCTGCTTTGGCTTTAGGGCTTGCATATCACTAACATATATCTCA 1177
DB 1060 AAGAGTATATATGCTGCTTTGGCTTGCCTGCGGATCGCAATCAATTTAATCAATATCTCA 1119
QY 1178 GAGATGTAGAGAGAGATGCGAGAGAGAGAGAGATTTACTTGGCTCAAGTGAATTAGCAC 1237
DB 1120 GAGATGTAGAGAGAGATGCGAGAGAGAGAGAGATTTACTTGGCTCAAGTGAATTAGCAC 1179
QY 1238 AGGCAAGGCTCTCCGAGAGACATATTTGCTGAGAGAGTGACTGATTAAGTGAAGACT 1297
DB 1180 AGGCAAGGCTCTCCGAGATGATATTTGCTGAGAGGCTGACCGATTAATGAGAGACT 1239
QY 1298 TTAGTGAAGAAACAAATTCAGAGGCGAGAGAAATCTTTTATGATGATGAGAGAGAGTGTCA 1357
DB 1240 TTAGTGAAGAAACAAATTCAGAGGCGAGAGAAATCTTTTATGATGAGAGAGAGAGGCTGTA 1299

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QY 1358 CAGACTGCACTCTGCTAGTAGATGAGCGCTGTGTTAAGCGCGCTGTGTATGCAAGA 1417
DB 1300 CAGATTTAGCTCAGCTAGTAGATGATCCCTGTATGGGCACTTTGTGTATACGCAAAA 1359
QY 1418 TATTGAGAGATTTGAAGCCCAAGCACTACCAACTTACAGAGAGGCTTATGTAGCA 1477
DB 1360 TACTAGATGAGATTTGAAGCCCAATGATACCAACTTACCAAGAGAGCAATATGTAGCA 1419
QY 1478 AGCCAAAGAGCTTCTCACTTGGCCCATTTGCTTATGCAAAATCTTTGGCCCTATA 1537
DB 1420 AATCAAGAGATTTGATGATTTACTTATTTGATGCAAAATCTTTGTGCTCTTACAA 1479
QY 1538 GAATCTCTCTCCACTAGCAAGA 1561
DB 1480 AACTGCTCTCTTCAAGATATA 1503

RESULT 8
AA012495
ID AA012495 standard; cDNA; 1646 BP.
XX
AC AA012495;
XX
DT 25-MAR-2003 (updated)
DT 18-SEP-1991 (first entry)
XX
DE Tomato fruit ripening related gene pTOM5.
XX
KM ripening; lycopene; transgenic tomato; ss.
OS Lycopersicon esculentum var. Alisa Craig.
FH Key location/Qualifiers
FT CDS 201..1436
FT /*tag= a
FT
PN W09109128-A.
XX
XX 27-JUN-1991.
PD
XX
PF 10-DEC-1990; 90WO-GB01924.
XX
PR 13-DEC-1989; 89GB-0028179.
XX
PA (ICL) IMPERIAL CHEM IND PLC.
XX
PI Bird CR, Grierson D, Schuch W;
XX
DR WPI, 1991-208154/28.
XX
PT DNA construct to modify synthesis of plant carotenoid(s) -
PT comprises sequence homologous to gene of clone pTOM5 preceded by
PT plant promoter
XX
XX
PS Disclosure; Fig 1; 35pp; English.
XX
CC Clone pTOM5 was derived from a cDNA library isolated from ripe
CC tomato RNA (Stater et al., Plant Molecular Biology 5, 137-147,
CC 1985). The protein it encodes is estimated to have mol. wt. ca.
CC 48kD. pTOM5 is expressed in ripening fruit. Strongest expression is
CC at the full orange stage of ripening; no expression is detected in
CC green fruit. See also AA012494.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1646 BP; 529 A; 249 C; 387 G; 481 T; 0 other;

Query Match 48.6%; Score 840.4; DB 12; Length 1646;
Best Local Similarity 74.3%; Pred. No. 1.2e-229;
Matches 1221; Conservative 0; Mismatches 331; Indels 92; Gaps 9;

QY 101 TATATTCGTTGAATTAAGTGAATGACTCTAGAGATATCTTAC--AAGTATGCTTTT 157
DB 53 TAAATTTGTTGAGAGTGAATATATCTCTAGTGGAAATCTACTAGAGATATTTATTTT 112

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OY	158	TGATPAAATAGCTGAGGTGAGGAAGGTAACTPAAAGGAAACAAAAAATTGGAAATTGT	217
Db	113	CTATPAACTTAAGTAAAGTTTGGAAGGTAC- AAAAAAGAAACAAAAATTGGAAATTGT	171
OY	218	TTTAGACCAACCGAGGTTCTTGTTTCATGACCATGTCTGTTCGTTGTTGGTTGTT	277
Db	172	TTTAGACCAACAAGT---TTTCTTGCTCAGAAATCTCTGTCCTTGTATGGGTGT	228
OY	278	CTCCCACTTCCGAGGTCTCGAATGGGACAGGATTTGGATTCAGTCCGAGAGAAACC	337
Db	229	CTC---CTTGGACGCTCTCAATGGGACAGATTTCAATGATCATGTCGGAGGAGAAACC	285
OY	338	GGGTCTTTGTATCATTCGAGGTTCTAGTCTCAGATAGGAATTTGATGTGGAAATGGAGAA	397
Db	286	GTTTTTTTTGATTCATTCAGG-----CATAGGAATTTGGGTCTCATAGAGAA	333
OY	398	TCAAGAAAGTGGGAGACAAAGGTGAATTTTGCTCTTAAATTCATCAGATCAAGATATT	457
Db	334	TCAATNAGGT-----	344
OY	458	CATGCTTGGGTGATCAAGAACTGAAAAAGGAAAGCATTTCTGTACAGTCCAGTTTGG	517
Db	345	-----GGTGGAAAGCAACTATATATGACCGGAATTTTCTGTACGTCCTCATTT	396
OY	518	TGCGTAGCCCACTGAGGAAATGACTGTGTCTATCAGAGAAAAAGGTGATATGTGTAT	577
Db	397	TGGCTACTCCATCTGGAGAACGGACGATGACATCGAACATAGTCTATATGTGTGT	456
OY	578	TAAAGCAGACAGCTTTAGTGAAGAGGAGCGCTGAGATCTACCGATGATTTAGAGTGAAC	637
Db	457	TGAGCGACAGACGCTTGGTGAAGAGGCACTGAGATCTAACATGATGATTAAGTGAAC	516
OY	638	CGGATATTGTGTTCCAGGGAATTTGGCTTTGTAAGTGAAGCATATGATGTTGTGGCG	697
Db	517	CGGATATATCTATTTCCGGGGAATTTGGCTTTGTAAGTGAAGCATATGATGATGTGGTG	576
OY	698	AAATATGTGCAAGATATGCAAAAGCATTTTACTTNGAACCAAGCTAATGACCCOAGAA	757
Db	577	AAATATGTGCAAGATATGCAAAAGCATTTTAACTTNGAACATATGATGATCTCCGAGA	636
OY	758	GAAAGAGCGATCTGGGCAATATATGTGTGTGAGAGAAACGATNAGCTGTGTATG	817
Db	637	GAAAGAGGCGATCTGGTCAATATATGTGTGTGAGAGAAACGATNAGCTGTGTATG	696
OY	818	GCCCTAATGCACTCCACATAACTCCGCAAGCTTTTGAATGGTGGGAGACACAGCTGAAAG	877
Db	657	GCCCAAGCATCATATATATATACCCGGGAGCTTGAATAGGTGGGAAAAATAGCTAGAAAG	756
OY	878	ATATTTTCAGTGGGGGCGCATTTGATATGCTTGAATGCTGCTTATCCGANTACTGTCCCA	937
Db	757	ATGTTTTCATATGGGGGCGCATTTGACATGCTGATGATGCTTGTGCCATACAGTTCTA	816
OY	938	GATTTCTGTTGATATTCAGCCATTCAAGATATGATGAAGAAATGGTATGGAATTGT	997
Db	817	ACTTTCACGTTGATATTCAGCCATTCAAGATATGATGAAGAAATGGTATGGAATTGA	876
OY	998	GGAATTCAGATACAAAACCTTTCGATGAGCTATATCTGTATTTGTTACTATGTCGTGTA	1057
Db	877	GAAATTCAGATACAAAACCTTTCGAGCACTATATCTTATTTATTTATGTGCTGTA	936
OY	1058	CTGTAGATTGATGATGTTCCAGTTATGAGTATGCACTGATCAAAAGCAACAACAG	1117
Db	937	CGTTGGGTGATGATGTTCCAAATTAATGGGATGCGCCCTGAATCAAAAGCAACAACAG	996
OY	1118	AGAGTGTATATATGCTGCTTTGGCTTTAGGGCTTGCAATCACTAAACAATATACTCA	1177
Db	997	AGAGGTATATATATGCTGCTTTGGCTTGGGATGCAAAATCAATTAATACTAATACTCA	1056
OY	1178	GAGATGTGGAAGAAATGCGCAAGAAAGGAAGATATCTTGCGTCAAGATGAATTAAGAC	1237
Db	1057	GAGATGTGGAAGAAATGCGAAGAAAGGAAGATATCTTGCTTCAAGATGAATTAAGAC	1116

QY	1238	AGGCAAGGCGCTCCGACGAAAGACATATTTGCTGGAAAGTCACTGATTAAGGAGAACT	1237
Db	1117	AGCGAGGCTCTATCCGATGMAAGATATATTTGCTGSAAGGCTGACCGATTAATGAGAAATCT	1176
QY	1298	TTATGAAGAAACAAATTCAGAGGGCGAGAAATTCCTTGATGAGTCAGAGAAAGTGTCA	1357
Db	1177	TTATGAAGAAACAAATTCATAGGGCAAGAAAGTTCCTTGATGAGGACAGAAAGGCGTGA	1236
QY	1358	CAGAACTGGACTCGCTAGTAGATGAGCGCTGCTGTAAACGCGCTGCTGTGATGSCAAGA	1417
Db	1237	CAGATTTAGCTCAGCTGATGATGATTCCTGTATGGGCATCTTTGCTCTTGATCCGCAAAA	1296
QY	1418	TATTGACGAGATTGAAGCCCAACGACTACAAACCTTCACAGAGAGGCTTATGTTAGCA	1477
Db	1297	TACTAGATGAGATTGAAGCCAAATGACTACAAACCTTCACAAAGAGACATATGTGAGCA	1356
QY	1478	AGCCAAAG-AGCTTTCACCTTGGCCATGTCCTATGCAAAATCTCTTGSCCCCTAT	1536
Db	1357	AATCAAGCAAGTTGATGTGACTATACCTATGTCATATGCAAAATCTCTTGSCCTTCA	1416
QY	1537	AGAACTTCTCTCCACTAGCAAAAGACATGATGAAAGTAGTGAATCAATGAGTATTATAC	1596
Db	1417	AAATCGCCTCTTCAAAAGATTAAGCATGAAGATGAAATATATATATATATATAGC	1476
QY	1597	ACT-----AAGAAACTCAGGTACTGTGAATGAGATATCTTTGCTATAAGTGTAT	1648
Db	1477	AATGTACATTAGAAAGAAAAAAGAGAGAAAGTGTGTATGATGATTAAGATATAT	1536
QY	1649	CATCAAAAGTAGATGTGT-----AAATGCAATATGCAAAATCTCTTGAGAAATATTTCTCC	1704
Db	1537	CATAAATATTTAGTGTGTAGTAACATTCAAATTAATATATCTCTTGAGTGTGTATCTTC	1586
QY	1705	ACACTCATCAACCCCTCAAGTAG	1728
Db	1597	ACTTATCTCAACTCTTTGAGAG	1620

XX	RESULT 9	
XX	AAV03879	
XX	ID	AAV03879 standard; cDNA; 1316 BP.
XX	AC	
XX	AAV03879;	
XX		
DT	29-APR-1998	(first entry)
XX		
DE	Phytoene synthase coding sequence from N. benthamiana.	
XX		
KW	Phytoene synthase; transgenic plant; enhanced carotenoid synthesis.	
KW	ultra violet absorbder; food colour; sg.	
XX		
OS	Nicotiana benthamiana.	
XX		
FH	Key	Location/Qualifiers
FH	CDS	1..1242
FT		/*tag= a
XX		
PN	US5705624-A.	
XX		
PD	06-JAN-1998.	
XX		
PF	27-DEC-1995;	95US-0579667.
XX		
PR	27-DEC-1995;	95US-0579667.
XX		
PA	(DELL/) DELLA-CIOPPA G R.	
PA	(FITZ/) FITZMAURICE W P.	
PA	(GRIL/) GRILL L K.	
PA	(HELL/) HELLMANN G M.	
PA	(KUMA/) KUMAGAI M H.	
XX		
PI	Della-Cioppa GR, Fitzmaurice WP, Grill LK, Hellmann GM;	
PI	Kumagai MH;	
XX		

DR MPI, 1998-086196/08.
 DR P-PSDB; AAM41058.
 CC DNA encoding tobacco phytoene synthase polypeptides - useful for
 PT producing recombinant polypeptides or transgenic plants
 PS Claim 1, Column 21-26; 25bp; English.
 CC This sequence encodes the phytoene synthetase from *Nicotiana benthamiana*.
 CC The phytoene synthetase coding sequence represents a cDNA of the
 CC invention. The isolated nucleic acid molecules are used for producing
 CC recombinant polypeptides or transgenic plants with enhanced ability to
 CC synthesise carotenoids. Phytoene has been used as a ultra violet absorber
 CC and other carotenoids have been used as food colours, animal feeds and in
 CC the pharmaceutical and cosmetics industries.
 XX
 XX
 SQ Sequence 1316 BP; 403 A; 221 C; 342 G; 350 T; 0 other;
 Query Match 46.9%; Score 811.2; DB 19; Length 1316;
 Best Local Similarity 80.2%; Pred. No. 2.5e-221;
 Matches 1039; Conservative 0; Mismatches 173; Indels 84; Gaps 4;
 QY 250 ATGCTGTTGCTTGTGTTGGTGTGTTCTCCCACTTCGAGGTCTCGAATGGACAGCA 309
 DB 1 ATGCTGTTGCTTGTGTTGGTGTGTTCTCCCACTTCGAGGTCTCGAATGGACAGCA 57
 QY 310 TTGTTGATTTCAGTCCGAGAGGAAACCGGCTTGTATTCATCCAGTTCTTACTGCA 369
 DB 58 TTCTTGATTCATCCGAGAGGAAACCGGCTTGTATTCATCCAGTTCTTACTGCA 105
 QY 370 GATGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 429
 DB 106 CATGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 165
 QY 430 GGCTCTTATTCGTGATCCAGATATTATGCTTGGTGATCAAGAACTGAAAAGGA 489
 DB 166 GGTTCTGTA----- 175
 QY 490 AGCACTTCTCTGTAAGTCCAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 546
 DB 176 -----AGTCTGTAAGTCCAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 219
 QY 547 TCATCAGAGAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
 DB 220 ACATCAGAGAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 279
 QY 607 CTGAGATCTACCGATATTTAGAGTGAACCGGATATTGTTGTTCCAGGAAATTTGGC 666
 DB 280 TTGAGATCTACCGATATTTAGAGTGAACCGGATATTGTTGTTCCAGGAAATTTGGC 339
 QY 667 TTGTTGAGAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
 DB 340 TTGTTGAGAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 399
 QY 727 TACTTGAAGCAAGCTAATGACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
 DB 400 TACTTGAAGCAAGCTAATGACCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 459
 QY 787 TGTGAG 846
 DB 460 TGTGAG 519
 QY 847 GCTTTAGATGAGTGGAG 906
 DB 520 GCTTTAGATGAGTGGAG 579
 QY 907 CTTGATGCTGTTTATCCGATATCTGTCAGATTTCTGTTGATATTCAGCATTCAGCA 966
 DB 580 CTCGATGCTGTTTATCCGATATCTGTCAGATTTCTGTTGATATTCAGCATTCAGCA 639
 QY 967 GATATGATGAG 1026
 DB 640 GATATGATGAG 699

QY 1027 CTATATCTTATTTGTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1086
 DB 700 CTATATCTTATTTGTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 759
 QY 1087 GGTATGCACTGTAATCAAGGCAACACAGAGAGTATATATGCTGTTGGCTTTA 1146
 DB 760 GGCATGCACTGTAATCAAGGCAACACAGAGAGTATATATGCTGTTGGCTTTG 819
 QY 1147 GGGCTTGCAATCACTAATCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1206
 DB 820 GGTATGCACTGTAATCAAGGCAACACAGAGAGTATATATGCTGTTGGCTTTG 879
 QY 1207 AGAGTATCTTCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1266
 DB 880 AGAGTATCTTCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 939
 QY 1267 GCTGAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1326
 DB 940 ACTGAGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999
 QY 1327 AATTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1386
 DB 1000 AAGTTCTTCAATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1059
 QY 1387 GTGTTAAGAGGCTGCTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1446
 DB 1060 GTATGAGAGTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1119
 QY 1447 AACCACTTCAAGAGAGGCTTATGTTAGCAAGCAAGAGAGAGAGAGAGAGAGAG 1506
 DB 1120 AACCACTTCAAGAGAGGCTTATGTTAGCAAGCAAGAGAGAGAGAGAGAGAGAG 1179
 QY 1507 GCTTATGCAAAATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1542
 DB 1180 GCTTATGCAAAATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1215
 RESULT 10
 AA299482
 ID AA299482 standard; cDNA; 1239 BP.
 XX
 AC AA299482;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE cDNA encoding a phytoene synthase polypeptide.
 XX
 KW Gibberellin acid; copalyl diphosphate synthase; 3beta-hydroxylase;
 KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
 KW seed germination; seedling growth; gibberellin biosynthetic pathway;
 KW transgenic plant; hypocotyl; epicotyl; ss.
 OS
 XX
 LYcopersicon esculentum.
 FH
 FT Key Location/Qualifiers
 FT CDS 1..1239
 FT /tag= a
 FT /product= "phytoene synthase"
 FT /transl_except= (pos: 1027..1029, aa: Lys)
 FT /transl_except= (pos: 1057..1059, aa: Arg)
 PN MO200009722-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 10-AUG-1999; 99WO-US18066.
 XX
 PR 10-AUG-1998; 98US-0096111.
 PR 07-JUN-1999; 99US-0137977.
 XX
 PA (MONS) MONSANTO CO.
 XX

PI Brown SM, Ellich TD, Heck GR, Kishore GM, Logusch EM, Logusch SJ;
 PI Piller KU, Rao S, Ream JE;
 XX
 DR MPI: 2000-224351/19.
 DR P-P8DB; AAY84101.
 XX
 PT Obtaining transgenic plant useful for controlling seed germination and
 PT seedling growth comprises transgene comprising a sequence expressing
 PT altered levels of an essential hormone
 XX
 PS Claim 45; Page 254-255; 267pp; English.
 XX
 CC The present sequence encodes a phytoene synthase polypeptide, which
 CC is used in the method of the invention. The specification describes
 CC methods for the inhibition and control of gibberellin acid levels.
 CC Gibberellin acid levels may be inhibited or controlled by use of
 CC a chimeric expression construct expressing a RNA or protein which
 CC suppresses the gibberellin biosynthetic pathway sequence, diverts
 CC substrate from the pathway, or degrades pathway substrates or products.
 CC The methods uses copalyl diphosphate synthase, 3beta-hydroxylase,
 CC 2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta-hydroxylase
 CC polynucleotides to achieve this. The method is used to control seed
 CC germination and seedling growth especially to regulate gene products of
 CC gibberellin biosynthetic pathway and restoration of normal seed
 CC germination, in transgenic plants. The plants produced are gibberellin
 CC deficient, and have shortened hypocotyl and/or epicotyl phenotypes
 CC compared to normal plants.
 CC
 XX
 SQ Sequence 1239 BP; 376 A; 208 C; 316 G; 339 T; 0 other;
 Query Match 46.7%; Score 806.4; DB 21; Length 1239;
 Best Local Similarity 83.5%; Pred. No. 5.7e-220;
 Matches 914; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 1066 TTGATGAGTGTCCAGTTATGGTATTCAGCTGATCAAGGCAACAGAGAGGTGTA 1125
 DB 745 TTGATGAGTGTCCAGTTATGGTATTCAGCTGATCAAGGCAACAGAGAGGTGTA 804
 QY 1126 TATATGCTGTTGGCTTTAGGCTTGAATCACTAACCAATATATCTCAGATGTA 1185
 DB 805 TATATGCTGTTGGCTTTAGGCTTGAATCACTAACCAATATATCTCAGATGTT 864
 QY 1186 GGAGAAATGCCAGAAAGGAGATGATCTGCTCAAGTAAATAGCACAGGAGG 1245
 DB 865 GGAGAAATGCCAGAAAGGAGATGATCTGCTCAAGTAAATAGCACAGGAGGT 924
 QY 1246 CTCTCCGACGAGACATATTTGCTGAAAGTGAATGATTAAGTGAAGAACTTTATGAG 1305
 DB 925 CTATCCGATGAAGATATATTTGCTGAAAGGTGACGATTAATGAGAACTTTATGAG 984
 QY 1306 AAACAAATTCAGAGGCGGAGAAATTTTGTATGATGATCAGAAAGGTTCACAACTG 1365
 DB 985 AAACAAATTCAGAGGCGGAGAAATTTTGTATGATGATGAGGAGAAATGCGTACAGAAATTG 1044
 QY 1366 GACTCTGTATGATGATGCGCTGTGTTAAACAGCGCTGCTGTTGATGCGCAAGATTTGGAC 1425
 DB 1045 AGCTCAGCTGATATATTTCCCTGTATGGGCAATCTTTGATCTGTACCGCAAAATATCTAGAT 1104
 QY 1426 GAGATGAGGCAACGACTACCAACACTTCAAGAGAGGCTTATGTTAGCAAGCCAAAG 1485
 DB 1105 GAGATGAGGCAACGACTACCAACACTTCAAGAGAGGCTTATGTTAGCAAGCCAAAG 1164
 QY 1486 AAGCTTCACTTTGCCATTTGCTTATGCAAAATCTTTGTGCCCCCTATAGAACTTC 1545
 DB 1165 AAGTTGATGATTAATCTATGATGATGCAAAATCTTTGTGCCCCCTATAGAACTTC 1224
 QY 1546 TCTCCTAGCAAA 1559
 DB 1225 TCTCCTAGCAAAATA 1238

RESULT 11
 AAD40272
 ID AAD40272 standard; cDNA; 1239 BP.
 XX
 AC AAD40272;
 XX
 DT 22-OCT-2002 (first entry)
 XX
 DE Tomato phytoene synthase cDNA.
 XX
 KW Gibberellin; transgenic plant; seed germination; seedling growth;
 KW transgenic; phytoene synthase; enzyme; GA; gene; tomato; ss.
 XX
 OS Lycopersicon esculentum.
 XX
 XX
 Key Location/Qualifiers
 FT CDS 1..1239
 FT /*Cag= a
 FT /product= "Phytoene synthase"
 FT /transl_except= (pos:1027..1029, aa:lys)
 FT /transl_except= (pos:1057..1059, aa:arg)
 XX
 XX US2002053095-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 10-AUG-1999; 99US-0371307.
 XX
 PR 10-AUG-1999; 99US-0371307.
 XX
 PA (BROW/) BROWN S M.
 XX
 PI Brown SM, Ellich TD, Heck GR, Kishore GM, Logusch EM, Logusch SJ;
 PI Piller KU, Rao S, Ream JE;

CC The present sequence encodes phytoene synthase 4. It was isolated from
CC a cDNA library prepared from mRNA extracted from the petals of Gentiana
CC lutea. The nucleic acid sequence was amplified from the library using
CC PCR primers AAV16952-53. The phytoene synthase gene is useful for
CC breeding plants with variable flower colours.

XX Sequence 2868 BP; 887 A; 499 C; 648 G; 833 T; 1 other;

Query Match 40.1%; Score 692.4; DB 19; Length 2868;
Best Local Similarity 73.6%; Pred. No. 3,4e-187;
Matches 949; Conservative 0; Mismatches 311; Indels 30; Gaps 4;

Qy 240 TTTCATGAGCATGCTGTTGCTTTGTTGCGGTTGTTCTCCACTTCGAGTCTGAA 299
Db 1390 TTCTGTAAACATGCTATTTGTAACGCTATGGTTGTTCCGCGAGTTCTGAAGTTTGA 449
Qy 300 TGGGACGAGATTGTTGATTCAGTCCGAGAGAAACCGCGCTTGTATCATCCAGTT 359
Db 450 TGGCAATGTTTCTTGGAGCCAAATTCGAGAAATTCATTTTCG----- 495
Qy 360 CCTAGCTGAGATAGGAATTTGATGTGGAATGGAGATCAAGAAAGGTGGAGACAAAG 419
Db 496 -----GATAAAGTTTATATATACATGGAAGAGTTAAGAAAGTTAAGACCAAG 545
Qy 420 GTGGAATTTGCTCTTAAATTTGCTGATCCAGATATTCATGCTTGGGTGATCAAGAC 479
Db 546 GCGTAGATCATGTTATGGGTTGAGATTGAGTTCAATTTGCTTGAAGAGTCTGAT 605
Qy 480 TGAAA--AGGGAACATTTCTCTGTACAGTCCAGTTTGGTGGTACCCAGCTGGGA 536
Db 606 AGAGCCCCGGGAAAGAAATTAATCGTATCCCGATTTATAGCTACCCGGCAGGAGA 665
Qy 537 AATGCTGTGTCATCAGAGAAAGAGTATGATGTGGATTTAAAGCAGCAGCTTAGT 596
Db 666 AATGACATGATGATAGAGCAAGAGTTTATGATTCGTTTAAAGCAGCAGCTTAGT 725
Qy 597 GAAGAGCAGCTGAGATTCAGATGATTAGAAAGTGAAGCCGATATTTGTTCCAG 656
Db 726 TAATAGACAGTTGAGCTTGAAGAAATTTGAGAGTGAACCGGACATTAATTTCCAG 785
Qy 657 GAATTTGGGCTTTGATGAGTGAAGCATATGATGTTGGCCGAGTATGTGACAGTATGC 716
Db 786 AAACGCGAAGCTTTGAATGAAGCTTATGATCGGTGAGAAAGTATGCTGAATATGC 845
Qy 717 AAAGCATTTTACTAGAGCAACAGCTATATGACCCAGAGAGAGAGAGAGCTATGAGC 776
Db 846 CAAGCATTTCTACTGAGGAAACCCAGCTATGACACCGAGAGCCCTTAACTATGAGC 905
Qy 777 AATATATGTGTGTGTCAGAGAGAACGATGAGCTTGTATGAGCCCTAATGATCCACAT 836
Db 906 GATATATGTATGTGTAGAGAGACAGATGAGCTTGTATGAGCCCTAATGAGTCAACAT 965
Qy 837 AACTCCGACAGCTTATGATAGTGGAGACACGAGCTGAGAAATATTTTCAGTGGCGGCC 896
Db 966 AAATCCAAACCGGTTAGAGTGGAGCAAGATTAAGATGTTTCAAGGGCAAC 1025
Qy 897 AATTGATATGCTTATGCTGCTTATCCGATATCTGTCCAGATTTCCGTTGATATCA 956
Db 1026 TTTTATATATGCTTATGCTGCTTATCTGATACATTCACAAATATCTGTGAGCATCA 1085
Qy 957 GCCATTCAGAGATATGATTAAGAGAAATGCTATGAGCTTGTGAATCCAGATCAAAAC 1016
Db 1086 GCCATTTAGAGATATGATTAAGAGAAATGCGATGATCTGAAGAAATGAGATTCAAA 1145
Qy 1017 TTTGATAGCTATATCTATTTTACTATGTTCTGTGATCTGTGATGATGATGAT 1076
Db 1146 TTTGATAGCTATATCTTATCTTATGCTATATGCTGTGCTGTACAGTTGCTGATAGT 1205
Qy 1077 TCCAGTTATGGGTATGAGACCGATCAAGGCAACACAGAGATGATATATATGCTGC 1136
Db 1206 ACCAGTATATGGGATGAGACCGGATCTAAGGCAACACAGAAATGTGTAATATGAGC 1265
Qy 1137 TTGGCTTTAGGGCTTGCAAAATCACTAACATATACTCAGAGATGTAGAGAAAGATGC 1196

Db 1266 TTATATCTTGGGATCCGGAACAGCTGACTAACTATTAAGGATGTTGAGAAAGATGC 1325
Qy 1197 CAGAGAGGAAGATATACCTTGCCTCAAGATGAATTAGCAACAGGAGGCTCCGAGCA 1256
Db 1326 AAGAGAGGAGAGGTGATCTTACTCAAGATGAATTAGCAACAGGAGGTTATCAGATGA 1385
Qy 1257 AGACATATTTGCTGAGAGATGACTGATTAAGTGAAGGACTTTATGAGAAACAAATTCA 1316
Db 1386 GACATTTTGTCTGAGAAATGTAACAAATGAGAGATTTTATGAGAAAGCAATCA 1445
Qy 1317 GAGGCGAGGAATTTCTTATGATGATGAGAAAGGTGTACAGAACTGACTTGC-TA 1375
Db 1446 AAGGCTGAGAAATTTCTATATGATGATGAGAAAGGATCCGAACTCAGCTCCGGA 1505
Qy 1376 GTAGATGCGCTGTTTAAAC--AGGCTGCTGTGATCGCAAGATATTGACAGATTTGA 1433
Db 1506 GCAATTTGCTGTGTGGCCAGCGCTTGTCTTTTATGAGAAATATGATGAGATGA 1585
Qy 1434 AGCCAAAGCTACAACTTCAACAGAGGCTTATGATGAGCAAGCCAAAGACTTCT 1493
Db 1566 AGCAATGACTACAACTTTCACAAAGGCTTATGTAACAGGCAAGAAAGTAT 1625
Qy 1494 CACCTGCCATTTGCTTATGCAAAATCTCT 1523
Db 1626 AGCTATGCTGTGATGATGCAAGTCTCT 1655

RESULT 13

AAV16949 ID AAV16949 standard; cDNA to mRNA; 1921 BP.

AC AAV16949;

DT 06-JUL-1998 (first entry)

DE Nucleic acid encoding phytoene synthase 2.

KW Phytoene synthase; breeding; variable flower colour; ds.

XX Gentiana lutea.

OS Gentiana lutea.

FT Key Location/Qualifiers

FT CDS 412..1689

FT /*tag= a

XX JPI0084966-A.

PD 07-APR-1998.

PF 17-SEP-1996; 96JP-0245107.

PR 17-SEP-1996; 96JP-0245107.

PA (IWAT-) IWATE KEN.

DR WPI: 1998-264853/24.

XX P-PSDB: AAW46962.

XX Phytoene synthase gene - useful for breeding plant of variable

PS flower colour

XX Claim 2; Pages 7-9; 15pp; Japanese.

CC The present sequence encodes phytoene synthase 2. It was isolated from

CC a cDNA library prepared from mRNA extracted from the petals of Gentiana

CC lutea. The nucleic acid sequence was amplified from the library using

CC PCR primers AAV16952-53. The phytoene synthase gene is useful for

CC breeding plants with variable flower colours.

XX Sequence 1921 BP; 633 A; 296 C; 438 G; 554 T; 0 other;

Qy Query Match 39.3%; Score 678.4; DB 19; Length 1921;

Best Local Similarity 72.4%; Pred. No. 2,8e-183;
Matches 924; Conservative 0; Mismatches 326; Indels 30; Gaps 3;

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OY 240 TTTCATGAGCATGTCGTTGCTTGTGTTGGGTTGTTGTTCCACATTCGAGGTCGCA 299
Db 402 TTCTGTAAACATGTCATATTTGTAAGCTTAAGGTTGTTGCGGAGTTCTGAAGTTTGAG 461
OY 300 TGGGACAGATTTGTTGATTCAGTCCGAGAGGAAACCGGTCCTTGTATCATCCAGTT 359
Db 462 TGGCAATGTTTCTTGGAGCAATTCGAGAAAGTTACATTTTTCG----- 507
OY 360 CCTAGCTCAGATAGGAATTTGATGTGGAATGGGAGAAATCAGAAAGTGGGAGCAAG 419
Db 508 -----GATAAAGTTTATGTACATGAGAGAGTTAAGAAAGTAGACACCAAG 557
OY 420 GTGGAATTTGGCTCTTAATGTCGATCCAGATATTCATGCTGGGTGAGATCAGAAC 479
Db 558 GGTGATACATCGTTATGGGTTGGAATTTGAGTTGATTTGCTTGAAGAGCTGGATT 617
OY 480 TGAAA-----AGGAGACACTTCTCTGTACAGTCCAGT--TTGGTGGCTAGCCAGCTG 533
Db 618 AAGAGACCCCGGAGAAAGATTATCGGTATCCCTCCAGATTTATAGCTACCCCGGAG 677
OY 534 AGAATGACTGTGTCAATCAGAGAAAAAGGTATGATGTGTAATTAACAGGACAGCTTT 593
Db 678 GGAATGACGATGACATCAGAGCAAAAGTTATGATGTGTTTAAAGCAAGCAGCTTT 737
OY 594 AGTGAAGAGGACGCTGATGATCCGATATTTGAAGAGGAAACCGGATTTGTTGTC 653
Db 738 GATTAATTAACAGTTAGGCTTGAAGAAAAATTTGGAGGTGAAACCGGACATTAATTTTGGC 797
OY 654 AGGGAATTTGGGCTTGTGATGAGAACATATGATCGTTGGGAGATATGTGACAGATA 713
Db 798 AAGAAACGGAACGTCCTTGAATGAAGCTTATGATCGGTGTCGAGAGATGTCTGAATA 857
OY 714 TGCAGAGACATTTACTTAAGAACCAAGCTATGACCCGAGAGAGAAAGAGCTATCTG 773
Db 858 TCCCAAGTCATTCCTACTGGGGGAAACAGCTCATGACCGAGAGAGCGTTAGCTATCTG 917
OY 774 GGCATATATGTGTGTGTCAGAGAGAACGATGAGCTTGTGATGAGCCCTAATGCAATCCA 833
Db 918 GCGCATATATGTGTGTGTCAGAGAGCAAGATGAGCTTGTGATGAGCCCTAATGCAATCCA 977
OY 834 CATTAATCCGAGCTTGTGATAGGAGGAGACCAAGCTGAGAAAGATTTTCAAGTGGG 893
Db 978 CATTAATCCGAGCTTGTGATAGGAGGAGCAAGATTTGAAGATGTTTCAAGTGGG 1037
OY 894 GCCATTGTATGCTGTGATGCTGCTTATCCGATACTGTCTCCAGATTTCTGTTGATAT 953
Db 1038 ACCTTTGATATGCTGTGATGCTGCTTATCTGATACCATTTACCAAGTATCTGTGACAT 1097
OY 954 TCAGCCATTCAGAGATATGATGAGAGATGCGTATGAGCTTGTGAAATCCAGATACA 1013
Db 1098 CCAGCCATTTAGAGATATGATGAGAGATGCGGATGATCTGAAGAAATCCGATACAA 1157
OY 1014 AACTTCGATGAGCTATATCTCATTTGTAATGTCGTGACTGTGAGATTGATGAG 1073
Db 1158 GAATTTTCAGAGCTGTATCTTACTGCTATTTATGTGCGCTGAGACGTTGCTGATGAG 1217
OY 1074 TGTTCAGTTATGGGTATGCACTGATCAAAAGGCAACAGAGAGTGTATATATGC 1133
Db 1218 TGTACCAAGTAATGGGATGCACTGATCTAAGGCAACAGAGAGTGTATATATGC 1277
OY 1134 TGTCTTGGCTTTAGGGCTTGCAAATTAACCAATATATCTCAGAGATGAGAGAGA 1193
Db 1278 AACTTTATCTTTGGGGATGCGCAACGAGCTGATTAACATTTCTAAGGATGTTGAGAGAA 1337
OY 1194 TGCAGAGAGAGAGAGATATGCTGCTCAGAGTGAATAGACAGAGGAGGCTCCGA 1253
Db 1338 TGCAGAGAGAGAGAGTGTACTACTCAAGATGAATTAAGCAACGAGTTTATCAAA 1397
OY 1254 CGAAGACATATTTGCTGGAAGAGTACTATAGTGAAGAACTTTATGAGAAACAAT 1313

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Db 1398 TGAGACATTTTTGCTGGAAGAAAGTTACAGACAAATGAGAGATTTTATGAGAGCAAT 1457
OY 1314 TCAGAGGGGAGAGAAATTTCTTATGATAGTCAGAGAAAGGTGTACAGAACTGAGCTGCG 1373
Db 1458 CAAGAGGGGTAAATAATTTATGATGATGACGAGAAAAAGGTCCCGGAATCAGCTCCGC 1517
OY 1374 TAGTATGAGCTGTGTATTAACAGCGCTGCTGTGTATGCAAGATATTTGAGAGATTGA 1433
Db 1518 GAGCAGATTTGCTGTGTGGGAGCGCTGCTTTTATAGAAAAATATTGATGAGATAGA 1577
OY 1434 ACCCAAGACTACAAACAATTCAAGAGAGGCTTATGTTAGCAACCAAGAGACTTCT 1493
Db 1578 AGCAATGACTACAAACAATTCACAAAAAAGGCTTATGTAAACAGAGCAAGAACTAT 1637
OY 1494 CACCTTGCCCATTTGCTTATGCAAAATCTCT 1523
Db 1638 AGCTATGCTGTAGCATGTGCCAAGTCTCT 1667

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RESULT 14

AAV16948
ID AAV16948 standard; cDNA to mRNA; 2085 BP.

AAV16948;

06-JUL-1998 (first entry)

Nucleic acid encoding phytoene synthase 1.

Phytoene synthase; breeding; variable flower colour; ds.

Gentiana lutea.

Key Location/Qualifiers

FT CDS 586..1866

FT FT. /*tag= a

PN JF10084966-A.

PD 07-APR-1998.

PF 17-SEP-1996; 96UP-0245107.

PR 17-SEP-1996; 96UP-0245107.

PA (IMAT-) IMATB KEN.

DR WPI; 1998-264853/24.

DR P-PSDB; AAW46961.

PT Phytoene synthase gene - useful for breeding plant of variable

flower colour

PS Claim 1; Pages 5-7; 15pp; Japanese.

XX The present sequence encodes phytoene synthase 1. It was isolated from

CC a cDNA library prepared from mRNA extracted from the petals of Gentiana

CC lutea. The nucleic acid sequence was amplified from the library using

CC PCR primers AAV16952-53. The phytoene synthase gene is useful for

CC breeding plants with variable flower colours.

XX

SQ Sequence 2085 BP; 654 A; 320 C; 479 G; 632 T; 0 other;

Query Match 38.8%; Score 670.4; DB 19; Length 2085;

Best Local Similarity 72.0%; Pred. No. 5.8e-181;
Matches 929; Conservative 0; Mismatches 331; Indels 30; Gaps 3;

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OY 240 TTTCATGAGCATGTCGTTGCTTGTGTTGGGTTGTTGTTCCACATTCGAGGTCGCA 299
Db 576 TTCTGTAAACATGTCATATTTGTAAGCTTAAGGTTGTTGCGGAGTTCTGAAGTTTGAG 635
OY 300 TGGGACAGATTTGTTGATTCAGTCCGAGAGGAAACCGGCTTTGTATCATCCAGATT 359

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Db	636	TGGCAATGTTTTCTTGAGGCCAATTGAGAAAGTTACATTTTTCG-----	681
OY	360	CCTAGCTGAGATAGAAATTTGATGTGAAATGGAGAAATCAAGAAAGTGGAGACAAAG	419
Db	682	-----GATAAAGTTTTAATGTACAAATGGAAGAGTTAAGAAAGATAGACACCAAG	731
OY	420	GTGGAATTTTGGCTCTTTAATTGTCGATCCAAATTCACAGCTTGGGGGATCAAGAAC	479
Db	732	GGGTGATCAGCTTATGGGGTTTGGAGATTTTGAGTTCAATTTTGCTTGAAGAGACTCTGAAAT	791
OY	480	TGAAA---AGGAAACACTTTTCTCTGTACAGTCCAGTTTGGTGGCTACCCAGCTGAGAGA	536
Db	792	AGAGACCCCGGGAAGAAAGATTATGGGGATACCTCCATATTAATAGTTAACCCCGGAGAGAG	851
OY	537	AATGACTGTGTCATCAGAGAAAAGGTGATGATGTGTTAATAAGCAGGACGCTTTAGT	596
Db	852	AAATACATGACATCAGAGCAAAAAGTTTATGATGTGCTTTTAAAGCAAGCAGCTTTGAT	911
OY	597	GAAAGGAGAGCTGAGATCTACCGATGATTTAAGTGAACCGGATATTGTTGTTCCAG	656
Db	912	TAAATGACAGTGAAGGCTTAGAGAAAATTTGGAGTGAACCGGACATTATTTTTCACAG	971
OY	657	GAATTTGGGCTTGTGAGTGAAGACATGATGTTGGCGCAAGATGTGACAGATATAC	716
Db	972	AAACCGCAACGTTTGATGAGAGCTTATGATCGGTGTGAGAAAGTATGTCTGAATATGC	1031
OY	717	AAAGACATTTTACTTAGAACCAACAGCTAATGACCCCAAGAGAGAAGAGTACTTCTGGGC	776
Db	1032	CAAGTCATTTCTACTGGGGGAAACCACTCATGACACCGGAGAGGCGTTTAGCTATCTGGGC	1091
OY	777	---AATATATGTGTGTGACAGAGAAACGATAGAGCTGTGATATGGCCCTAATGATCCCA	833
Db	1092	CGATATATATGATGATGCGTAGGAGACAGATATAGCTTTGTATGGGCGCTAACGCGTCA	1151
OY	834	CATAACTCCGCAAGCTTTAGATAGGTGGGAGACAGAGCTGGAAGATATTTTCACTGGGCG	893
Db	1152	CATAATTCACCCCGGTTAAGATAGGTGGGAGCAAGATCAGAAAGTGTTTTACAGGGCA	1211
OY	894	GCCATTGATATGCTTGAATGCTGCTTTATCCGATACTGTCTCCAGATTTCTGTGATAT	953
Db	1212	ACCTGTGATATGCTTGAATGCTGCTTTATCTGATCCATTAACAGTATCCTGTGATCAT	1271
OY	954	TCAGGCATTCAGAGATATGATTTGAAGGAATGGGTATGGAATGTGTGGAATCCAGATACA	1013
Db	1272	CCAGGCATTTAAGATATGATTAAGGAAGATGGGATGATCTGAAAGAAATCCAGATACAA	1331
OY	1014	AACTTCGATGAGCTATATCTGATTTGTTACTATGTTGGTGTACTGTAGATTTATGAG	1072
Db	1332	GAATTTCCATGACGCTGATCTTTACTGTATTAATGTGGCTGGACACAGTTGGCTTATGAG	1391
OY	1074	TGTTCCAGTTATGGGTATTTGCACTGAAATCAAGGCAACACAGAGAGTATATATATGC	1133
Db	1392	TGTACCAATTAAGGGCATTTGCACTGGAATCTAAGGCAACACAGAAAGTGTATGATGTC	1451
OY	1134	TGCTTTGGCTTTAGGGCTTGCAATTCACCTAACCAATATCTCAGAGATGTAGGAGAA	1193
Db	1452	AGCTTTATCTTTGGGGATTCGCCAACAGCTGTACTTAACATTTCTAAGGAGTGTGGAGAA	1511
OY	1194	TGCCGAAGAGAGAGATTACTTGGCTCAAAATGAAATTAGACAGGACGGGCTCCGA	1251
Db	1512	TGCAGAAAGAGAGAGGTGTACTTCACTCAAAATGAAATTTAGACAGAGGTTTATCAGA	1571
OY	1254	CGAAGACATTTTGTCTGAGAGAGTACGTGATAAGTGAAGAACTTTATGAGAAACAAT	1311
Db	1572	TGAGGACATTTTGTGTGGAAGATTTACAGACAAATGAGAGATTTTATGAAACAACAAT	1631
OY	1314	TCAGAGGCGCAGAGAAATTTTGTGATGAGTCAGAGAAAGGTGTCAAGAACTGGACTTGC	1377
Db	1632	CAAAAGGCGCTAAGAAATTTCTATGATGATGACAGAGAAAGAGTCCCGAACTCAGCTCCGC	1691
OY	1374	TAGTGAATGCGCTGTGTTTAAACAGCGCTGTGTGTTATGCAAGATATTTGAGAGAAATGA	1433
Db	1692	GAGCAGATTTGCTGTGTGGGACGCTGTGCTTTTATATAAAAAATTTGGAATGAATAGA	1751

QY	1434	AGCCAGCATTACAACAACCTTACAGAGAGGGCTTATGTTAGCAAGCCAAAGAGCTCT	1493
DB	1752	AGCAATGACTACACAACTTTGGCCAGAGGGCTTATGTAAACAGAGGGAAGAGCTATT	1811
QY	1494	CACCTTGCCATTGCTTATGCAAAATCTCT	1523
DB	1812	AGCTATGCTGTAGATATGCGCAAGTCTCT	1841

RESULT 15

ID	AAV16950 standard; cDNA to mRNA, 1932 BP.
XX	
XX	AAV16950;
AC	
XX	
DT	06-JUL-1998 (first entry)
XX	
DE	Nucleic acid encoding phytoene synthase 3.
XX	
XX	Phytoene synthase; breeding; variable flower colour; ds.
KX	
XX	
OS	Gentiana lutea.
XX	
Key	Location/Qualifiers
PH	499..1785
FT	CDS
FT	/*tag= a
XX	
FN	JPI0084966-A.

AA	07-APR-1998.	
PD		
XX	17-SEP-1996;	96JP-0245107.
PF		
XX	17-SEP-1996;	96JP-0245107.
PR		

XX (IWAT-) IWATE KEN.
PA
XX
DR WPI; 1998-264853/24.
DR P-PSDB; AAW46963.

PT Phytoene synthase gene - useful for breeding plant of variable
PT flower colour

PS Claim 3; Pages 10-12; 15pp; Japanese.

CC The present sequence encodes phytoene synthase 3. It was isolated from
CC a cDNA library prepared from mRNA extracted from the petals of *Gentiana*
CC *lutea*. The nucleic acid sequence was amplified from the library using
CC PCR primers AAV16952-53. The phytoene synthase gene is useful for
CC breeding plants with variable flower colours.

Sequence 1932 BP; 635 A; 302 C; 434 G; 561 T; 0 other;

Query Match	37.8%	Score 653.4	DB 19	Length 1932
Best Local Similarity	72.6%	Pred. NO. 4e-176		
Matches 940	Conservative 0	Mismatches 321	Indels 34	Gaps 6

QY	240	TTTATNAGGCAATGTCTGTGCTTTTGTGGGGTGTGTTCTCCACATCCGAGGTCTCGAA	299
Db	489	TTCTGTTAACATGTCTAATTTGTACGCTATGGGTGTGTTGCCGAGTCTGAAATTTTGAAG	548
QY	300	TGGGACAGAAATTTGTGATTCATGTCGGAAGAGAAACCGCGCTTTGTATCATCAGGTT	359
Db	549	TGGCAATGTTTTCTTGAGCCCAATTCGAGAAAGTTACCATTTTTTCG-----	594
QY	360	CCTAGCTCGAATAGGAATTTGATGTGGAAATGGGAAATCAAGAAAGTGGGAGCAAAAG	419
Db	595	-----GATTAAGTTTTATATGTACATGGAAGATTAAGAAAGTAGACACCAAAAG	644
QY	420	GTGGAATTTGGGCTTTTAATTGCTGATCCAAATATTCATGCTGGGTGATCAAGAAC	479
Db	645	GCGTAGATCACGTATATGGGGTTGGAGATTTGATGCTATTTCTTGAGAGAGTCTGGATTT	704

QY 480 TGAAG--AGGAGACACTTCTCTGTACAGTCCAGTTTGCTAGCCAGCTGAGAGA 536
DB 705 AGAGACCCCGGAGAGAAATATCGTATCTCCAGTATTAAGCTACCCCGGAGAGAGA 764
QY 537 AATGATCTGTGCATCAGAGAAAAGGTGATATGATGTGATTAAGCAGGCGCTTTAGT 596
DB 765 AATGACGATGACATCAGAGCAAAAGGTTATGATGTGCTTTTAAAGCAAGCCTTTGAT 824
QY 597 GAAGAGCAGCTGAGATCTACCGATGATTAGAGTAAAGCCGAGATATGTTGTTCCAGG 656
DB 825 TTAATGACAGTTGAGGTCTAGAGAAAATTGAGAGTGAACCGACATTAATTTGCCAGG 884
QY 657 GAATTTGGGCTTTGTTGAGTGAACATATGATCGTTGGCGAAGTATGTGACAGATATGC 716
DB 885 AAACCGAAGCGTTGTAATGAAGCTTATGATCGGTGTGAGAAATGATGTGTAATATGC 944
QY 717 AAAGCATTTTACTTAGAACCAGCTAATGACCCAGAGAGAGAAAGCTATCTGGGC 776
DB 945 CAAGTCATTCTAAGTGGGAAACCCAGCTCATGACACCGAGAGCGCTTTAGCTATCTGGGC 1004
QY 777 AATATATGTGTGTGACAGAGAAACGATGAGCTTGTGATGGCCCTAATGCATCCACAT 836
DB 1005 GATATATGTATGTGTAGAGAGACAGATGAGCTTGTGATGGCTTAACGCGTCAACAAAT 1064
QY 837 AACTCCGCAAGCTTTAGATAGGTGGGAGACAGGCTGGAAGATATTTTCAGTGGCGGCC 896
DB 1065 AAATCCAAACCGGTTAGATAGGTGGGAGCAAGATTAAGAGATGTTTCAAAAGGCAACC 1124
QY 897 AATTGATATGCTTGAATGCTGCTTTATCCGATATCTGTCTCCAGATTTCTGTTGATATTCA 956
DB 1125 TTTTATATATGCTTGAATGCTGCTTTATCTGATACCAATTAACAGTATCTGTGACATCCA 1184
QY 957 GCCATTGAGATATGATTAAGTGAATGCTATGAGACTTGTGAAATCCAGATACAAAC 1016
DB 1185 GCGATTGAGATATGATTAAGTGAATGCTATGAGACTTGTGAAATCCAGATACAAAC 1244
QY 1017 TTTTCATGAGCTATATCTCTATTTGTAATGTTGCTGCTGCTAGATGATGATGT 1076
DB 1245 TTTTCATGAGCTATATCTCTATTTGTAATGTTGCTGCTGCTAGATGATGATGT 1304
QY 1077 TCCAGTATGCTGATTTGCACTGGAATCAAAGGCAACACAGAGCTATATATGCTGC 1136
DB 1305 ACCAGTAAATGGGCAATGCACTGGAATCTAAGGCAACACAGAGCTATATATGCTGC 1364
QY 1137 TTTGGCTTAGGCTTGCATAATCACTAATCACTAATCACTAATCACTAATCACTAATCA 1196
DB 1365 TTTATCTTTGGGATCGCGAACCACTGCTAATCTTAAGGATGTTGGAGAAATGC 1424
QY 1197 CAGAAGAGAGAGATATCTGCTCAAGATGAATTAAGCAGGCGCTCCGACGA 1256
DB 1425 AAGAAGAGAGAGAGATGCTACCTCAAGATGAATTAAGCAGGCTTTATCAAGATGA 1484
QY 1257 AGACATATTTGCTGGAAGAGTGAATGAAGAGAACTTTATGAAGAAACAAATTCA 1316
DB 1485 GGACATATTTTGGTGAAGAAAGTTCCAGACAAATGAAGATTTTATGAAGAAACAAATCA 1544
QY 1317 GAGGCGGAGAAATCTTTGATGA-GTCAAGAGAAAGGTGTCAAGAACTGGA-CT 1374
DB 1545 AAGGCTGAGAAATCTTATGATGATGCCAGAAAGGTCCTCCGAACTCACTCCGCG 1604
QY 1375 AGTAGATGGCTGTGT---TAAACAGCGCTGCTGTTATCCAGATATTGACGAGAT 1430
DB 1605 AGCAGATGCTGTGTGTGGGCGAGCGTTGCTTTTATAGAGAAAATTTGATGAGAT 1664
QY 1431 TGAAGCCAAAGCTAACAACACTTC-ACAAGAGAGGCTTATGTAAGCAAGCCAAAGAAC 1489
DB 1665 AGAAGCAATATGCTAACAACAAATTTCAACAAAAGGCTTATGTAACAAAGCAAGAAC 1724
QY 1490 TTCTACCTTGCCCATGTGTTATGCAAAATCTCTT 1524
DB 1725 TATTAGCTATGCTGTAGCATGTGCCAAGTCTCTT 1759

Search completed: January 16, 2004, 01:16:29
Job time : 497 secs

Matches 1187; Conservative 0; Mismatches 255; Indels 96; Gaps 7;

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Oy 109 TTGAATTAGTGGATAGACTCTAGTGGATATCTACAAGATGTTTTTTGTAATAAATAG 168
Db 221 TAGACTTAGTGGGAATCTAGAGATATTTTTTTATTTTTTATTAATAATTA 280
Oy 169 GCTGAGTGAAGGTAACTATA-----GGAAGACAATAAATTGGGATTTT 220
Db 281 GCAGAGGAGGAGAAACAGAAAACAGAAATAGACAAAACCTTGGAAATGTTT 340
Oy 221 AGACCAAGAGGTTCTTGTTCATGACATCTCTGTTGTTGTTGTTGTTTCTC 280
Db 341 AGACCAAGAGGTTTGTGTTTC---AGATGTCCTGTTGCTTGTATGAGTTGTTTAC 397
Oy 281 CCACTTCGAGGTTCTGATGGAGAGATTTGTGATTCAGTCCGAGAGAAACCGG 340
Db 398 ---CTTGTGAGGTTCTCAATGGAGACAGATTTTGTGATTCAGTAAAGAGGAGAAACCGG 454
Oy 341 TCTTGTATCATCCAGGTTCTAGCTCGAGATGAGATTTGATGTAATGGAGATCA 400
Db 455 TTTTGTACTCGTGCAGG-----CATAGGAATTTAGTGTGCAATGAGAGATCA 502
Oy 401 AGAAGGTGGAGAGACAAAGGTGGAATTTTGGCTCTTTAATGCTGATCCAGATTTCA 460
Db 503 AAGAGGTGTGAAACAAAGGTGGAATTTTGG-----533
Oy 461 GCTTGGGTGATCAAGAACTGAAAGGGAAGCACTTCTCTGTACAGTCCAGTTGGTG 520
Db 534 -----TTCGTACGCTGTGCGATGGTG 556
Oy 521 CTAGCCAGCTGAGAAAT---GACTGTGTATCAGAGAAAAGGTGATGATGTGAT 577
Db 557 CTACACCAACGGGAGAAATGGGCAATGACATCAGAACAGAGTTTATGATGTGAT 616
Oy 578 TAAAGCAGGACCTTTAGTGAAGAGCGAGCTGAGATCTACCGATATTTAGAAAGTGAAC 637
Db 617 TGAACCAAGACCTTTAGTGAAGAGCGAGCTGAGATCTACCGATATTTAGAAAGTGAAC 676
Oy 638 CGGATATTGTTGTCAGGGAATTTGGGCTGTTGATGGAAGCATGATGTTGGTGCG 697
Db 677 CGGATATCCCTCTCCCGGGAATTTGAGCTGTGTAAGTGAAGCATATGATGATG 736
Oy 698 AAGTATGTCAGAGATGCAAAAGACATTTTACTTAGAACCAAGCATTAATGACCCAGAGA 757
Db 737 AAGTATGTCAGAGATGCAAAAGACATTTTACTTAGAACCATGATGATGATGATG 796
Oy 758 GAAAGAGCTATCTGGGCAATATATGTGTGTGCAAGAGAACGATGAGCTTTGTTGATG 817
Db 797 GAAAGAGGCTATTTGGGCAATATATGTGTGTGCAAGAGAACGATGAGCTTTGTTGATG 856
Oy 818 GCCCTAATGCATCCCACTACTCCGCAAGCTTTGATAGTGGGAGACCAAGGCTGGAG 877
Db 857 GCCGAATGCATCATATATCTCCCAAGCTTTGATAGTGGGAGACCAAGGCTGGAG 916
Oy 878 ATATTTTCAGTGGGCGCATTTGATGATGCTTGTATGCTTTATCCGATACCTGCTCCA 937
Db 917 ATGTTTCAGTGGGCGCATTTGATGATGCTGATGCTGCTTTGTCGATACTGTTTCC 976
Oy 938 GATTTCTGTTGATATTCAGCCATTCAGAGATGATGAAAGAAATGGGATGAGCTTGT 997
Db 977 AGTTTCCAGTGTATTCAGCCGTTCCAGAGATGATGAAAGAAATGGGATGAGCTTGA 1036
Oy 998 GGAATCCAGATACAAACTTTCGATGAGCTATCTGATTTGATGATGCTGCTGTA 1057
Db 1037 GGAAGTCAAGATACGAAACTTTGATGAGCTATGCTTATGTTGATTAACGTGTGTA 1096
Oy 1058 CTGTAGATGATGAGTGTTCAGATTTAGGATTTGACCTGATCAAGAGCAACAAG 1117
Db 1097 CGGTTGGTGTATGATGTTCCATTAATGAGGATTTGACCTGATTCAAAGCAACAAG 1156
Oy 1118 AGAGTATATATGCTGCTTTGGCTTTAGGCGTTGCAATCACTAAACAATATCTCA 1177
Db 1157 AGAGTATATATGCTGCTTTGGCTTTAGGCGTTCGAAATCACTAAACAATATCTCA 1216

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Oy 1178 GAGATGTAGAGAGATGCCAGAGAGAGATATCTTGCTTCAAGATGAATTAGCAC 1237
Db 1217 GAGATGTAGAGAGATGCCAGAGAGAGATATCTTGCTTCAAGATGAATTAGCAC 1276
Oy 1238 AGCAGGAGCTCTCCGAGAGACATATTTGCTGGAAGAGTACTGATTAAGAGAACT 1297
Db 1277 AGCAGGAGCTCTCCGAGAGATGACATTTTCTGGAAGAGTACTGATTAAGAGAACT 1336
Oy 1298 TTATGAAGAAACAATTCAGAGGCGAGAAATCTTGATGAGTCAAGAGAGTGTCA 1357
Db 1337 TTATGAAGAAACAATTCAGAGGCGAGAAATCTTGATGAGTCAAGAGAGTGTCA 1396
Oy 1358 CAGAACTGAGCTCTGCTAGTATGATGAGCTGTGTTAAGAGGCTGCTGTTATGCAAGA 1417
Db 1397 CAGAACTGAGCTCTGCTAGTATGATGAGCTGTGTTAAGAGGCTGCTGTTATGCAAGA 1456
Oy 1418 TATTTGACGAGATTTGAAGCCAGACTTACAACTTCAAGAGAGGCTTATGTTGCA 1477
Db 1457 TACTGACGAGATTTGAAGCCAGACTTACAACTTCAAGAGAGGCTTATGTTGCA 1516
Oy 1478 AGCCAAAGAGCTTCTGACCTTGCCTTGCCTTATGCAAAATCTTGTGCCCTPATA 1537
Db 1517 AACCAAGAGCTTATTTCTTACTTATGCTTATGCAAAATCTTGTGCCCTPATA 1576
Oy 1538 GAACT-TCTCTCCACTAGCAAGAGACATGAGTGAAGTGTGATGATTTATAC 1596
Db 1577 GAACTCTTGCTCAGCTCTAGTGAAGCATGACATCAGAAATTAATTAACGAGAAAGCA 1636
Oy 1597 ACTAAGAACTCAGTACTTGTATGATGATCTTT 1634
Db 1637 TATATTTATTTATTTATGCTTTAAAGAAAGATTT 1674

```

RESULT 2

US-08-579-667-1

; Sequence 1, Application us/08579667

; Patent No. 5705624

GENERAL INFORMATION:

APPLICANT: Fitzmaurice, Wayne P.

APPLICANT: Hellmann, Gary M.

APPLICANT: Grill, Laurence K.

APPLICANT: Kumagai, Monte H.

APPLICANT: Della-Cioppa, Guy R.

TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN

TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESS: Virginia C. Bennett

STREET: 1211 East Morehead Street, PO Drawer 34009

CITY: Charlotte

STATE: No. 5705624th Carolina

COUNTRY: USA

ZIP: 28234

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/579,667

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Bennett, Virginia C.

REGISTRATION NUMBER: 37,092

REFERENCE/DOCKET NUMBER: 627-196

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-420-2200

TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1795 base pairs

TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 362..1591
 US-08-579-667-1

Query Match 49.7%; Score 858.6; DB 1; Length 1795;
 Best Local Similarity 76.4%; Pred. No. 8.4e-237;
 Matches 1230; Conservative 0; Mismatches 274; Indels 107; Gaps 10;

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QY 141 TACAGATATGCTTTTATATAAATAGCTGAGTGAAGATACA-----TAAAG 193
DB 248 TAAATTATTTATTTTATATAAATTAGAGAGGAGGAGAAACAAAACTGAAAG 307
QY 194 GAAAGACAAAACTTGGGAATGTTTACACCCGAGGTTCTTGTTTCATGACATGT 253
DB 308 TAGACAAAAAACCTTGGAAATGTTTACCAACCAAGCTTTTC--TTGCTCAGATGT 365
QY 254 CTGTTGCTTGTGTTGGGTTGTTTCCACCTTCGAGGCTCGAATGGGACAGATTC 313
DB 366 CTGTTGCCCTGTTATAGGTTGTTAC--CTTGAGGCTCTCAATGGGACAGATTC 422
QY 314 TGGATTCACTCCGAGAGGAAAACCGGCTTTGTATCATCCAGTTCTTAGCTCGAGATA 373
DB 423 TGGATTCAATTCGGGAGGAAACCGGCTTTTGATTGTCCAGGT-----ATA 470
QY 374 GGAATTTGATGTGGAATGGGAGATCAGAAAAGTGGGAGACAAAGTGGAAATTTGGCT 433
DB 471 GAAATTTGATGTGCAATGAGAGGAAACAGAGAGTGGGAAACAAAGTGGAAATTTGG-- 528
QY 434 CTTTAATGCTGATCCAAATATATCATGCTTGGGTGATCAAGAACTGAAAAGGAGACA 493
DB 529 ----- 528
QY 494 CTTTCTCTGTACAGTCCAGTTTGTGGCTAGCCACAGCTGAGAAAT---GACTGTGTAT 550
DB 529 ----TTCTGTAGTGTCTGTATGCTGTACACCCGGGAGAAATGGGACAGATGACAT 584
QY 551 CAGAGAAAAAGGTATGATGTGTTATTAAGCAGGACCTTTAGTGAAGGACAGCTGA 610
DB 585 CAGAACAGATGTTATGATGTGTTTAAACAAGCAGCTTTAGTGAAGGACAGTTGA 644
QY 611 GATCTACCATGATTTTGAAGTGAAGCCGAGATTTGTTCCAGGAAATTTGGCTGT 670
DB 645 GATCTACCATGATTTTGAAGTGAAGCCGAGATCCCTCTCCAGGCAAAATTTGAGCTGT 704
QY 671 TGAGTGAAGCATATGATCTGTGGGAGATATGTGACAGATATGCAAAAGACATTTTACT 730
DB 705 TGAGTGAAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 764
QY 731 TAGAACCAAGCTAATGACCCAGAGAGAAAGAGCTATCTGGGCAATATATGTGTGT 790
DB 765 TAGAACCAAGCTAATGACCTCCAGAGAGAAAGGCTATTTGGGCAATATATGTGTGT 824
QY 791 GAGAGAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 850
DB 835 GAGAGAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 884
QY 851 TAGATAGGTGGAGACGAGCTGGAAGATATTTTCAAGTGGGGGCAATTTGATGCTTG 910
DB 885 TAGATAGGTGGAGACGAGCTGGAAGATATTTTCAAGTGGGGGCAATTTGATGCTTG 944
QY 911 ATGCTGCTTTATCCGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 970
DB 945 ATGCTGCTTTATCCGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1004
QY 971 TGATTTGAAGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1030
DB 1005 TGATTTGAAGGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1064

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QY 1031 ATCTCTATTTGTTACTATGTTGCTGTGATCTAGATTTGATGATGATGATGATGATGAT 1090
DB 1065 ACCATATATTTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1124
QY 1091 TTGACCTTGATCAAGGCAACACAGAGATGATATATATGCTGCTTTGGCTTTAGGCT 1150
DB 1125 TTGACCTTGATCAAGGCAACACAGAGATGATATATATGATGATGATGATGATGATGAT 1184
QY 1151 TTGCAATCACTAACATATATCTCAGAGATGATGAGAGAAAGTCCAGAGAGAGAAAG 1210
DB 1185 TAGCAATCACTAACATATATCTCAGAGATGATGAGAGAAAGTCCAGAGAGAGAAAG 1244
QY 1211 TATACCTGCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1270
DB 1245 TCTATTTACCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1304
QY 1271 GAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1330
DB 1305 GAAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1364
QY 1331 TCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1390
DB 1365 TCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1424
QY 1391 TAAACGCTGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1450
DB 1425 GGGCTTCTTCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1484
QY 1451 ACTTCAAGAGAGGCTTATGTTAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1510
DB 1485 ACTTCAAGAGAGGCTTATGTTAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1544
QY 1511 ATGCAAAATCTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1569
DB 1545 ATGCAAAATCTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1604
QY 1570 AAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1618
DB 1605 TCAATTTTAAATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1664
QY 1619 TAAATGATATCTTTTGTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1677
DB 1665 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1724
QY 1678 ACAATCTTGTGTAGATAT--TTTCTCAGACTCATCAAACTTCAAGTGA 1727
DB 1725 ACAATCTTGTGTAGATATCTTAAACAATCTTAAACCTTCAAGGGA 1775

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RESULT 3

US-08-579-667-7
 ; Sequence 7, Application US/08579667
 ; Patent No. 5705624
 ; GENERAL INFORMATION:
 ; APPLICANT: Fitzmaurice, Wayne P.
 ; APPLICANT: Hellmann, Gary M.
 ; APPLICANT: Grill, Laurence K.
 ; APPLICANT: Kumagai, Monto H.
 ; APPLICANT: Della-Cioppa, Guy R.
 ; TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
 ; TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Virginia C. Bennett
 ; STREET: 1211 East Morehead Street, PO Drawer 34009
 ; CITY: Charlotte
 ; STATE: No. 5705624th Carolina
 ; COUNTRY: USA
 ; ZIP: 28234
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

TITLE OF INVENTION: DERIVED THEREFROM
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cushman, Darby & Cushman
 STREET: 1615 L Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20036-5601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/995,950
 FILING DATE:
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/625,664
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Kokulis, Paul N.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: PNK/3893/82895/MCM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944
 TELEX: 248453 cush
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1646 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 JS-07-995-950-2

QY 1649 CATCAAAAGTAGATTGT-----AAATTCATATGACAACTCTGTGTAGAAATATTTCTCC 1704
 Db 1537 CATAAATATATGTGTAGTAGACATTCATTAATATCTCTGTGTAGTGTGTATCTTC 1596
 QY 1705 ACACACTCAATCAACCTCAAGTGAG 1728
 Db 1597 ACTTATCTCAACTCTTTTGAGAG 1620

RESULT 5

US-08-300-582-2

; Sequence 2, Application US/08300582
 ; Patent No. 5750865
 ; GENERAL INFORMATION:
 ; APPLICANT: BIRD, COLIN R.
 ; APPLICANT: GRIERSON, DONALD
 ; APPLICANT: SCHUCH, WOLFGANG W.
 ; TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS
 ; TITLE OF INVENTION: DERIVED THEREFROM
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/300,582
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/859,523
 ; FILING DATE: 12-AUG-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 3893/95874
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 861-3000
 ; TELEFAX: (202) 822-0944
 ; TELEX: 6714627 CUSH
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1646 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-08-300-582-2

Query Match 48.7%; Score 842; DB 1; Length 1646;

Best Local Similarity 74.3%; Pred. No. 4.8e-232; Indels 92; Gaps 9;

Matches 1222; Conservative 0; Mismatches 330;

QY 101 TATAATCGTTGAATAATTAGTAGATGACTCTAGTAGATATCTAC--AAGTATGGTTT 157
 Db 53 TAATTTCTTTGAGAGTGGAATATCTCTAGTGGAACTTACGAGTATTTATTTT 112
 QY 158 TGAATAAATAGGCTGAGTGAGAGTAACTAAAGAAACAAAACCTTGGGAATGT 217
 Db 113 CTATTAACCTAAGTAAAGTTTGGAGGTGACA-AAAAGAAACAAAACCTTGGGAATGT 171
 QY 218 TTTGACACACGAGGTTCTTGTTCATGAGAGTCTGTTGTGTGGGTGTTT 277
 Db 172 TTTTGAACAACCAAGGT--TTTCTTGTCTCAAGATGTCTGTGCTTGTATGGGTGTTT 228
 QY 278 CTCACACTTCGAGGTCTCAAGATGGAGACAGATGTTGTGATTCAGTCCGAGAAGAAAC 337

Db 229 CTC---CTGTGACGTCTCAAAATGGGACAAATTTCATGGAATCAGTCCGGAGGAAACC 285
 QY 338 GCGCTTTTATATCATCCAGCTTCTAGTCTGAGATGGAAATTTGATGGAAATGGAGAA 397
 Db 286 GTTTTATGATTCATTCAGG-----CATAGAAATTTGTGTCCAAATGAGGAA 333
 QY 398 TCAAGAAAGGTGGAGACAAAGGTGGAATTTGGCTCTTTAAATGTGATCCAAATATT 457
 Db 334 TCAATAGAGT----- 344
 QY 458 CATGCTGGGTGATCAAGAACTGAAAAGGAAACCTTCTCTGTCAGTCCAGTTGG 517
 Db 345 -----GGTGAAGAACAACTAATATGAGACGGAATTTCTGTACGCTCTGCTATT 396
 QY 518 TGGCTAGCCAGGCTGGAGAAATGACTGTCTCATACAGAAAGGATGATGTTGTTAT 577
 Db 397 TGGCTACTCATCTGGAAACGAGCATGACATCGAACACAGATGCTTATGATGTGTTT 456
 QY 578 TAAAGCAGCAGCTTTAGTGAAGAGCAGCTGAGATCTACCGATGATTTGAAGTGAAGC 637
 Db 457 TGAGGACGAGCAGCTTGTGTGAAGAGCACTGAGATCTACATGATTTGAAGTGAAGC 516
 QY 638 CGGATATGTTGTTCCAGGGAATTTGGGCTTTGAGTGAAGCATGATGCTTTGGCG 697
 Db 517 CGGATATACCTAATTCGGGGAATTTGGGCTTTGAGTGAAGCATGATGAGTGTGTTG 576
 QY 698 AAGTATGCAAGATATGCAAGAACTTTACTTAGGAACCAAGCTAATGACCCAGAGA 757
 Db 577 AAGTATGCAAGATATGCAAGAACTTTACTTAGGAACCAAGCTAATGACCCAGAGA 636
 QY 758 GAAGAAGCTATCTGGGCAATATATGTGTGTGTCAGAGAAACGATGACTTGTGTATG 817
 Db 637 GAAGAAGCTATCTGGGCAATATATGTGTGTGTCAGAGAAACAGATGACTTGTGTATG 696
 QY 818 GCCCTAATGATCCACATATCTCCGACCTTTAGATGAGTGGAGACCAAGCTGGAAG 877
 Db 697 GCCCAACGATCATATATTAACCCCGACCTTTAGATGAGTGGAGAAATGAGCTGAGAG 756
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 Db 757 ATGTTTCAATGGGCGGCTTTGATGATGATGCTTTGATGATGCTTTGATGATGCTTT 816
 QY 938 GATTTCTGTTGATATTCAGCCATTCAGATATGATTTGAAGAAATGCTGATGACTTGT 997
 Db 817 ACTTTCAGTTGATATTCAGCCATTCAGATATGATTTGAAGAAATGCTGATGACTTGT 876
 QY 998 GGAATTCAGATCAAAAACCTTTCAGTATGCTATATCTTATGTTATGTTGCTGTGTA 1057
 Db 877 GAAATTCAGATCAAAAACCTTTCAGTATGCTATATCTTATGTTATGTTGCTGTGTA 936
 QY 1058 CTGAGATTTGATGAGTGTCCAGTTATGGTATTTGCACTGAAATCAAAAGCAACACAG 1117
 Db 937 CGTTGGTGTGATGAGTGTCCAGTTATGGTATTTGCACTGAAATCAAAAGCAACACAG 996
 QY 1118 AGAGTATATATATGCTGTTTGGCTTTAGGCTTGCATAATCACTAACCAATATCTCA 1177
 Db 997 AGAGCTATATATGCTGTTTGGCTTGTGGATTCGGAATTCATTAATCACTAATCTCA 1056
 QY 1057 GAGATGTTGAGAAATGTCAGAAAGGAGAAAGATCTACTTCTCAAGATGAATTTAGCAC 1116
 Db 1238 AGGAGGCTCTCCGACGAAAGATATATTTGCTGGAAGAGTGAATGATGAGAGAACT 1297
 QY 1117 AGGAGGCTCTATCCGAGGAAGATATATTTGCTGGAAGGAGTGAATGAGAGAACT 1176
 Db 1298 TTAATGAAGAACAATTCAGAGGCGAGAAATCTTGTATGATGTCAGAAAGGTGTCA 1357
 QY 1177 TTATGAAGAAACAATTCATAGGCGAAGAAAGTCTTTGATGAGGAGAGAAAGCGTGA 1236
 Db 1358 CAGAACTGACCTGCTAGTATGATGAGCTGCTGTAAACAGGCTGCTGTATGCAAGA 1417

Db 1237 CAGAAATGAGCTCAGCTAGTAAATTCCTGTATGGGACCTTTGGTCTTGTATCCGCAAAA 1296
 Qy 1418 TATTGGACGAGATTGAAGCCCAACGACTACAACTTCCAGAGAGGGCTTATGTTAGCA 1477
 Db 1297 TACTGATGAGATTGAAGCCCAATGACTACAACTTCCAGAGAGATATGAGAGA 1356
 Qy 1478 AGCCAAAG-AAGCTTCTCACTTGGCCATGTTTATGCAAAAATCTTTGCCCCCTAT 1536
 Db 1357 AATCAAGAGAGTATGATTCATTAATGCTATGCAATGCAAAATCTTTGCTCTTACA 1416
 Qy 1537 AGAATCTCTCTCCAGCTAGCAAAAGATGAAAGTATGAGTATGATCAATGATTAATAC 1596
 Db 1417 AATGCTCTCTCTTCAAAAGATGAAAGTATGAAATATATATATATATATATATAC 1476
 Qy 1597 ACT-----AAAGAACTCAGTACTGTATATGATATCTTTGCTTAATGCTAT 1648
 Db 1477 AATGATCATTAAGAAAAAGAAAGAAATGTTGTTGATGATATATATATATATAT 1536
 Qy 1649 CATCAAAAGTATGTTGT-----AATTCATATGACATCTCTTGTAGAAATATTTCTCC 1704
 Db 1537 CATTAATATTAAGTTGTTAGTAAATCATTAATATATATCTCTTGTAGTTGTTATCTTC 1596
 Qy 1705 ACATCATCAAACTCTCAAGTAC 1728
 Db 1597 ACTTATCTCAACTCTTGTAGAG 1620

RESULT 6

US-09-180-342-2
 ; Sequence 2, Application US/09180342A
 ; Patent No. 6239331
 ; GENERAL INFORMATION:
 ; APPLICANT: Drake, Caroline R.
 ; APPLICANT: Bird, Colin R.
 ; APPLICANT: Schuch, Wolfgang W.
 ; TITLE OF INVENTION: Enhancement of Gene Expression
 ; FILE REFERENCE: SEB0156
 ; CURRENT APPLICATION NUMBER: US/09/180,342A
 ; EARLIER FILING DATE: 1998-11-05
 ; EARLIER APPLICATION NUMBER: PCT/GB97/01414
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: UK 9611981.3
 ; EARLIER FILING DATE: 1996-06-07
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1239
 ; TYPE: DNA
 ; ORGANISM: Lycopersicon esculentum
 US-09-180-342-2

Query Match 46.9%; Score 811.2; DB 3; Length 1239;
 Best Local Similarity 83.8%; Pred. No. 3e-223;
 Matches 917; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 466 GGTGATCAAGAACTGAAAGGAGCACTTCTGTACAGTCCAGTTGAGGCTAGC 525
 Db 145 GGTGAAAGCAATATATATATGACGCAATTTTCTGTAAGGCTGCTATCT 204
 Qy 526 CCAGCTGAGAAATGATCTGTCTATCAGAGAAAAGTGTATGATGTGATATTAAGCAG 585
 Db 205 CCATCTGAGAGAGCGACGATGACATCGAAGAGATGTCTATGATGTGTTTGGAGCAG 264
 Qy 586 GAGCTTTAGTAAAGGAGCGAGTATGATCTACCGATGATTAGAAAGTGAAGCCGATAT 645
 Db 265 GAGGCTTGTGTAAAGGAGCGAGTATGATCTACCGATGATTAGAAAGTGAAGCCGATAT 324
 Qy 646 GTTGTTCAGGGAATTTGGGCTTTGTTAGTGAAGCATATGATGTTGTCGGAAGATAT 705
 Db 325 CCTATTTCCGGGGAATTTGGGCTTTGTTAGTGAAGCATATGATGTTGTCGGAAGATAT 384
 Qy 706 GGAGATATGAAAGCATTTTACTTAGAACCAAGCTAATGACCCGACAGAGAAAGAA 765

Db 385 GCAGATGATGCAAGACGTTTAACTTAAAGAACTATGCTAATGATCTCCGAGAGAAAG 444
 Qy 766 GCTATCTGGGCAATATATGTTGTTGAGGAGAAACGATGAGCTTTGATGGCCCTAT 825
 Db 445 GCTATCTGGGCAATATATGTTGTTGAGGAGAAACGATGAGCTTTGATGGCCCTAT 504
 Qy 826 GCATCCCAATTAATCTCCCAAGCTTTAGATAGTGGAGAACGAGCTGGAAGATATTTTC 885
 Db 505 GCATCATATATTAATCCCGGAGCCTTATAGTGGAGAAATAGCTGAGAAATGTTTTC 564
 Qy 886 AGTGGCGGCAATTTGATATGCTGTATGCTCTTTATCCGATCTCTCTCAAGTTTCT 945
 Db 565 AATGGCGGCAATTTGATATGCTGTATGCTCTTTATCCGATCTCTCTCAAGTTTCT 624
 Qy 946 GTTATATTCAGCAATTAAGATATGATTTGAAGAAACGATAGCTTTGAGAAATCC 1005
 Db 625 GTTATATTCAGCAATTAAGATATGATTTGAAGAAACGATAGCTTTGAGAAATCC 684
 Qy 1006 AGATCAAAACTTTCGATGAGCTATATCTATTTGTTACTATGTTGCTGTTACTAGTA 1065
 Db 685 AGATCAAAACTTTCGATGAGCTATATCTATTTGTTACTATGTTGCTGTTACTAGTA 744
 Qy 1066 TTGATGAGTGTTCAGATTATGAGTATGTCACCTGATCAAGCAACAGAGAGTGA 1125
 Db 745 TTGATGAGTGTTCAGATTATGAGTATGTCACCTGATCAAGCAACAGAGAGTGA 804
 Qy 1126 TATATGCTGCTTTGAGCTTTAGGGCTTGCATATCACTAACCATATATCTAGAGATGA 1185
 Db 805 TATATGCTGCTTTGAGCTTTAGGGCTTGCATATCACTAACCATATATCTAGAGATGA 864
 Qy 1186 GGAGAAAGTGCAGAGAGAGAAAGTATCTTGCCTCAAGATGATTTAGCAAGGAGAG 1245
 Db 865 GGAGAAAGTGCAGAGAGAGAAAGTATCTTGCCTCAAGATGATTTAGCAAGGAGAG 924
 Qy 1246 CTCTCCGAGAGACATATTTGCTGGAAGAGTATGATGATGAGAGAACTTTATGAG 1305
 Db 925 CTATCCGATGAGATATATTTGCTGGAAGAGTATGATGATGAGAGAACTTTATGAG 984
 Qy 1306 AAACAAATTCAGAGGCGAGAGAAATCTTTGATGATGATGAGAGAAAGTGTCAAGATG 1365
 Db 985 AAACAAATTCAGAGGCGAGAGAAAGTCTTTGATGATGAGAGAGAGGTTCAAGATG 1044
 Qy 1366 GACTCTGCTAGTATGAGTGCCTGTGTAAACAGCGCTGCTGTGTATGCAAGATTTGAG 1425
 Db 1045 AGCTGAGTATGATATTTCCCTGTATGAGCACTTTTGTGCTTGTATCCGAAATATGAT 1104
 Qy 1426 GAGATGAGAGCAAGCACTTACACAACTTCAAGAGAGGCTTATGTTAGCAAGCCAAAG 1485
 Db 1105 GAGATGAGAGCAAGCACTTACACAACTTCAAGAGAGGCTTATGTTAGCAAGCCAAAG 1164
 Qy 1486 AAGCTTTCACCTTGGCCATTTGCTTATGCAAAATCTTGTGCCCCCTAATGAACTTCC 1545
 Db 1165 AAGTGTATGATTAATCAATGATGCAATGCAAAATCTTGTGCCCCCTAATGAACTTCC 1224
 Qy 1546 TCTCCACTAGCAAA 1559
 Db 1225 TCTCTCAAGATA 1238

RESULT 7

US-08-579-667-3
 ; Sequence 3, Application US/08579667
 ; Patent No. 5703624
 ; GENERAL INFORMATION:
 ; APPLICANT: Fitzmaurice, Wayne P.
 ; APPLICANT: Hellmann, Gary M.
 ; APPLICANT: Grill, Laurence K.
 ; APPLICANT: Kumagai, Monto H.
 ; APPLICANT: Della-Cioppa, Guy R.
 ; TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:

LENGTH: 1239
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
 US-09-180-342-1

Query Match 24.0%; Score 415.2; DB 3; Length 1239;
 Best Local Similarity 61.6%; Pred. No. 1.9e-109;
 Matches 663; Conservative 0; Mismatches 413; Indels 0; Gaps 0;

466 GGTGATCAAGAACTGAAAAGGAGACCTTTCTCTGTCAGTCCAGTTTGGCTACG 525
 145 GGAGGTAAACAGACAAACACGCTGAAAGTTCTCAGTTAGATCAGCAATCCTTGACACA 204
 526 CCAGCTGGAGAAATGCTGTGTCATCAGAAAAGGCTATGATGTTGTTAATAAGCG 585
 205 CTTACGGGTGAGAGACTATGACTACGCGCAAAATGTTGACAGCTGCTACTTCTGTCAA 264
 586 GCAGCTTTAGTGAAGAGCGAGCTGAGATCTACCGATTTAGAAAGTGAAGCCGATATT 645
 265 GGTGACTAGTAAAGTCAAGTATGAGTACGTAAGCACTTGAGTTAACTGACANT 324
 646 GTTGTCCAGGGAATTTGGGCTTTGTTGAGTGAAGCATATGATGTTGGCGAAGTATG 705
 325 CCAATACCTGGAACCTTGAGACTTCTTCTGAGGCTTACGACAGATGCGAGAGGTTTGC 384
 706 GCAGAGTATGCAAGACATTTTACTAGGAACCAAGCTAATGACCCGAGAGAAAGAGA 765
 385 GGAGAAATGCTAAACCTTCAATTTGGTACCATGTTGATATACACCAAAAGGCGTCTG 444
 766 GCTATCTGGGCAATATATGTTGTCGACAGAGAACGATGAGCTTTGATGGCCCTAAT 825
 445 GGAATATGGGCTATTATACGTTTGGTGGCGCTACTGACGATGATGAGACGACTAAT 504
 826 GCATCCCAATAACTCCGCAAGCTTTAGATGAGTGGGAGACCAAGCTGAGAAATTTTC 885
 505 GCTAGTTACATTAACACCCGCTGCTCTTGACAGATGGAGAACCGTTTGGAGACGTTT 564
 886 AGTGGCGGCGCATTTGATATGCTGTGATGCTGTTATCCGATACGTCCTCCAGATTTCT 945
 565 AACGGACGCTTTTGATATGTTGACGAGAGACCTTAGGACACTGTGAGCAATTTCCCT 624
 946 GTTGAATTTACGCCATTCAGATATGATTTGAAGAAATCGTATGAGACTTTGGAATTC 1005
 625 GTGACATCCACCTTTTGGGACATGATCGAGGCGATAGATGATTTTGTAACTT 684
 1006 AGATACAAAATTTTGATGAGCTATATCTTATTTGTTACTATGTTGCTGTGTA 1065
 685 CATTATAGAAATTTGATGAGTGTATTTGTACTGCTACTACGTGGCAGGAACCGTGGGC 744
 1066 TTGATGAGTGTCCAGTATGAGTATGCACTGTAATCAAAGCAACAGAGAGTGA 1125
 745 CTTATGCTAGTCCCTATCATGGAATTGACACAGAGAGTAAAGCTACTAATCTGTT 804
 1126 TATATGCTGCTTTTGGCTTTAGGGCTTGCAATCACTAACAATATATCTGAGATGTA 1185
 805 TACACCGAGCACTAGCATTTAGGTATAGCTAACGCTTACAAATATCTTGAGGAGCGTG 864
 1186 GGAGAGATGCGAGAGAGAAAGATATATCTTGCTCAAGATGAATTCACAGGCGAGG 1245
 865 GGTGAGAGCGACGTAGGGGTGCTGTGTATCTCCACAGAGCAGAGCTGCTCAAGCTGGA 924
 1246 CTCCTCGAGAGAGACATATTTGCTGAGAGAGTGAAGTATGAGAGAACTTTTGAAG 1305
 925 TTGAGTTCAGAGAGACATTTTCCAGGTGCTGTGTTACAGACAGTGAAGATTTTTCATGAAA 984
 1306 AAACAATTCAGAGGGCGAGAAATCTTGATGAGTGAAGAAAGGTCTCAGAGACTG 1365
 985 AAGCATTCACCGTCTGTAAATTTTTCAGAGAACTGAAAAGGAGATTTCTGAGCTT 1044
 1366 GACTGTGATGATGAGTGGCTGTGTTAACAGGCTGCTGTTGATCGCAAGATATTGAGC 1425

Db 1045 TCTAGTCATCAGAGTTTCCAGTTTGGCCAGCCTTGCTCTATAGAAAGATTTTGAC 1104
 Oy 1426 GAGATTGAAGCAACAGCATACAACTTCAAGAGAGGCTTATGTTAGCAAGCAAG 1485
 Db 1105 GAATTCGAGGCTTAAGCATTAATTAATTTTCTAAGCTGCTTACGTTTCTTAAGAGCAA 1164
 Oy 1486 AAGCTTCTACCTTGCCCATGCTTATGCAAAATCTCTTGCCGCCCTAATAGAAC 1541
 Db 1165 AAACCTTATGCTCTTCCAAATCGCTTAAGCTTAAGAGCTTGTTCCACCAACTAAGAC 1220

RESULT 9
 US-08-579-667-9
 ; Sequence 9, Application US/08579667
 ; Patent No. 5705624

GENERAL INFORMATION:
 APPLICANT: Fitzmaurice, Wayne P.
 APPLICANT: Hellmann, Gary M.
 APPLICANT: Grill, Laurence K.
 APPLICANT: Kumagai, Monto H.
 APPLICANT: Della-Cioppa, Guy R.
 TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
 TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Virginia C. Bennett
 STREET: 1211 East Morehead Street, PO Drawer 34009
 CITY: Charlotte
 STATE: No. 5705624th Carolina
 COUNTRY: USA

ZIP: 28234
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/579,667
 FILING DATE:

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Bennett, Virginia C.
 REGISTRATION NUMBER: 37,092
 REFERENCE/DOCKET NUMBER: 627-196
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-420-2200
 TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 749 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-08-579-667-9

Query Match 10.0%; Score 172; DB 1; Length 749;
 Best Local Similarity 65.7%; Pred. No. 1.2e-39;
 Matches 393; Conservative 0; Mismatches 110; Indels 95; Gaps 6;

Oy 109 TTGAATATGAGATAGACTCTAGTGATATCTCAAGATATGTTTGTATATAAATAG 168
 Db 226 TAGACTCTAGTGGGAATCTATGAGAGTATTTTATTTTATTTTATATAATTA 295
 Oy 169 GCTGAGTGAAGATAATTA-----GGAAAGACAAAACCTTGGAAATTTGTTT 220
 Db 296 CGAGAGGAGGAGAAAGAAACAGAAAACAGAAAGTAAGACAAAACCTTGAATTTGTTT 355
 Oy 221 AGACCAAGGAGTTTCTTGTTCATGAGCATGCTGTTGCTTTGTGTGGGTGTTTCTC 280
 Db 356 AGACAAACCAAGTTTGTGTTTC--AGAAATGCTGTGTCCTTGTATGAGGTGTTTAC 412
 Oy 281 CCATTCGAGGTCTCGAATGGAACAGATTTGTTGATTCAGTCCGAGAAAGAAACCGCG 340

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Db      413  ---CTTGGAGGTCCTCAATGGGACAGATTCTTGATTCAGGAAGGAGGAAACCGGG 469
Oy      341  TCTTGTATCAATCCAGGTTCTTCAAGTCAAGATAGAAATTTGATGTGAATGGAGAAATCA 400
Db      470  TTTTGTACTCGTCGGG-----CATGGAAATTTAGTGTGATGATAGAGAAATCA 517
Oy      401  AGAAAGTGGGAGCAAAAGTGTGAATTTGGCTCTTATTTGCTGATCAAGATATTCAT 460
Db      518  AAAGAGGTGTGAACAAAGTGTGAATTTGG----- 548
Oy      461  GCTTGGGTGATCAAGAACTGAAAAGGAGACCTTTCTGTACAGTCCAGTTGGTGG 520
Db      549  -----TTCCGTACGGTCTCGATGTGG 571
Oy      521  CTAGCCGAGCTGGAGAAAT---GACTGTGATCAACAGAAAAGGTGATATGTGTAT 577
Db      572  CTACACCAACGGGAAATGGGACAAATGACATCAGAACAGAAAGTTTATGATGTGTAT 631
Oy      578  TAAAGCAGGAGCTTTAGTGAAGAGCAGCTGAGATCTACCGATGATTTAGAGTGAAGC 637
Db      632  TGAACCAAGCAGCTTATGATGAAAAGGACGCTGAGATCTACTGATGATTTAGAGTGAAGC 691
Oy      638  CGGATATTTGTTTCCAGGGAATTTGGCTGTGAGTGAAGCATATGATCGTTGGTGG 695
Db      692  CGGATATCTCTCTCCCGGGAATTTGAGCTGTGTAAGTGAAGCATATGATGATGTAG 749

```

RESULT 10
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/993,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMUN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

IMMEDIATE SOURCE:
CLONE: pTZgpl-Fls
US-08-232-463-14

Query Match 3.1%, Score 54; DB 1; Length 7218;
Best Local Similarity 3.1%, Pred. No. 2.8e-05;
Matches 12; Conservative 223; Mismatches 153; Indels 0; Gaps 0;

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Oy      1093  GCACCTGAATCAAGGACAGACAGAGTGTATATATGCTGCTTGTAGGCTT 1152
Db      1445  GAATTTGTCACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1386
Oy      1153  GCAATCACTAACCAATATATCTAGAGATGTAGAGAGATGCCAGAGAGAGTA 1212
Db      1385  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1326
Oy      1213  TACTTGCTCAAGATGATTAAGCAGAGGAGGCTCTCCAGCAAGACATATTTGCTGA 1272
Db      1325  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1266
Oy      1273  AGAGTACGTATAGTGAGAGGAACTTATGAGAAACAATTCAGAGGAGGAAATTC 1332
Db      1265  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1206
Oy      1333  TTGTATGATCAGAGAAAGGTGTACAGAACTGACTCTGTAGATGAGCTGTGTA 1392
Db      1205  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1146
Oy      1393  ACAGCGCTGCTGTTGATTCGCAAGATATTGACAGATTTAAGCCAAAGCTACACAC 1452
Db      1145  RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1086
Oy      1453  TTCACAGAGAGGCTTATGTTGCAAGC 1480
Db      1085  RRRRRRRRRRRRRRRRRRRATCGCAGC 1058

```

RESULT 11
US-08-260-546-10

Sequence 10, Application US/08260546
Patent No. 5922602

GENERAL INFORMATION:
APPLICANT: Kumagai, Monte H.
APPLICANT: della-Cioppa, Guy R.
APPLICANT: Donson, Jonathan
APPLICANT: Harvey, Damon A.
TITLE OF INVENTION: The Cytoplasmic Inhibition of Gene
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2710 Sand Hill Road
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,546
FILING DATE: 16-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8129-086-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIR

```

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..114
US-08-260-546-10

Query Match
Best Local Similarity 79.8%; Score 52.4; DB 2; Length 114;
Matches 75; Conservative 0; Mismatches 16; Indels 3; Gaps 1;

QY 245 TGAGATGTCCTGCTTGTGTTGGGTTGTTCTCCACCTCCGAGGTTCTGATGGGA 304
DB 23 TAAATATGTCGTGCTGCTGTTGATGCGTTGTTCTC---CTTGTGACGCTTCAAAATGGGA 79

QY 305 CAGATTGTGATTCAGTCCGAGGAAGAACCG 338
DB 80 CAGTTTCATGGAATCAGTCCGGAGGGAACCG 113

RESULT 12
US-09-436-068A-12
; Sequence 12, Application US/09436068A
; Patent No. 6376752
; GENERAL INFORMATION:
; APPLICANT: KUMAGAI, MONTO H.
; APPLICANT: della-CIOPPA, GUY R.
; APPLICANT: DONSON, JONATHAN
; APPLICANT: HARVEY, DAMON A.
; APPLICANT: GRILL, LAURENCE K.
; TITLE OF INVENTION: THE CYTOPLASMIC INHIBITION OF GENE
; FILE REFERENCE: 008010086US02
; CURRENT APPLICATION NUMBER: US/09/436,068A
; PRIORITY FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 09/265,576
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/260,546
; PRIOR FILING DATE: 1994-06-16
; PRIOR APPLICATION NUMBER: 08/184,237
; PRIOR FILING DATE: 1994-01-19
; PRIOR APPLICATION NUMBER: 07/923,692
; PRIOR FILING DATE: 1992-07-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Tomato mosaic virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128) ... (114)
US-09-436-068A-12

Query Match
Best Local Similarity 79.8%; Score 52.4; DB 4; Length 114;
Matches 75; Conservative 0; Mismatches 16; Indels 3; Gaps 1;

QY 245 TGAGATGTCCTGCTTGTGTTGGGTTGTTCTCCACCTCCGAGGTTCTGATGGGA 304
DB 23 TAAATATGTCGTGCTGCTGTTGATGCGTTGTTCTC---CTTGTGACGCTTCAAAATGGGA 79

QY 305 CAGATTGTGATTCAGTCCGAGGAAGAACCG 338
DB 80 CAGTTTCATGGAATCAGTCCGGAGGGAACCG 113

RESULT 13
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US-09-265-576-12
; Sequence 12, Application US/09265576
; Patent No. 6479291
; GENERAL INFORMATION:
; APPLICANT: KUMAGAI, MONTO H.
; APPLICANT: della-CIOPPA, GUY R.
; APPLICANT: DONSON, JONATHAN
; APPLICANT: HARVEY, DAMON A.
; APPLICANT: GRILL, LAURENCE K.
; TITLE OF INVENTION: THE CYTOPLASMIC INHIBITION OF GENE
; FILE REFERENCE: 008010086US02
; CURRENT APPLICATION NUMBER: US/09/265,576
; PRIORITY FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/436,068
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: 09/265,576
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/260,546
; PRIOR FILING DATE: 1994-06-16
; PRIOR APPLICATION NUMBER: 08/184,237
; PRIOR FILING DATE: 1994-01-19
; PRIOR APPLICATION NUMBER: 07/923,692
; PRIOR FILING DATE: 1992-07-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Tomato mosaic virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (128) ... (114)
US-09-265-576-12

Query Match
Best Local Similarity 79.8%; Score 52.4; DB 4; Length 114;
Matches 75; Conservative 0; Mismatches 16; Indels 3; Gaps 1;

QY 245 TGAGATGTCCTGCTTGTGTTGGGTTGTTCTCCACCTCCGAGGTTCTGATGGGA 304
DB 23 TAAATATGTCGTGCTGCTGTTGATGCGTTGTTCTC---CTTGTGACGCTTCAAAATGGGA 79

QY 305 CAGATTGTGATTCAGTCCGAGGAAGAACCG 338
DB 80 CAGTTTCATGGAATCAGTCCGGAGGGAACCG 113

RESULT 14
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; PRIORITY FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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Qy 706 GCAGAGTATGCAAAACATTTTCTTAGAGAA CCAAGCTAATGACCCCGAGAGAGAAAGA 765
Db 385 GCAGAGTATGCAAAACGTTTAACTTAGAAGCTATGCTAATGACTCCCGAGAGAAAGG 444
Qy 766 GCTATCTGGGCAATATATGTGTGTGTGCGAGGAAACGATGAGCTTTGTGATGGCCCTTAT 825
Db 445 GCTATCTGGGCAATATATGTGTGTGTGCGAGGAAACGATGAGCTTTGTGATGGCCCAAC 504
Qy 826 GCATCCCAATATCTCCGCAAGCTTTAGATAGTGTGGAGACCAAGCTCGAAGATATTTTC 885
Db 505 GCATCAATATATTAACCCCGGAGCCCTAGATAGGTGGAAAAATAGGCTAGAAAGTGTTC 564
Qy 886 AGTGGGCGGCAATTTGATATGCTGTGATGCTGCTTTATCCGATCTGCTCCAGATTTCT 945
Db 565 AATGGGCGGCAATTTGATGATGCTGCTGCTGCTTTGTCCGATACAGTTTCTAACCTTCCA 624
Qy 946 GTTGATATTCAGCCATTCAGAGATATGATTTGAGAGAAATGCGTATGAGCTTTGGAATCC 1005
Db 625 GTTGATATTCAGCCATTCAGAGATATGATTTGAGAGAAATGCGTATGAGCTTTGGAATCC 684
Qy 1006 AGATACAAAACCTTCGATGAGCTATATCTATTGTTACATATGTTGCTGTGACTGTAGGA 1065
Db 685 AGATACAAAACCTTCGAGCACTATACCTTTATTTGTTATATGTTGCTGTGAGGTTGG 744
Qy 1066 TTGATGAGTGTTCAGATTATGAGTATGCACTGATCMAAGCAACAGAGAGTGT 1125
Db 745 TTGATGAGTGTTCAGATTATGAGTATGCCCCGTGATCMAAGCAACAGAGAGTGT 804
Qy 1126 TATATATGCTGCTTTGGCTTTGAGGCTTGCAATCACTAACCAATATATCTAGAGATGA 1185
Db 805 TATATATGCTGCTTTGGCTTGAGGAGTCCCAATCACTAACCAATATATCTAGAGATGT 864
Qy 1186 GGAGAGATGCGCAGAGAGAGAGATATCTTGCTCAAGATGATTTAGCAGAGAGG 1245
Db 865 GGAGAGATGCGCAGAGAGAGAGATCTATCTTGCTCAAGATGATTTAGCAGAGAGG 924
Qy 1246 CTCTCCGACGAAACATATTTGCTGGAAGAGTGAAGTGAATGAGAGAACTTTATGAG 1305
Db 925 CTATCCGATGAAGATATATTTGCTGGAAGAGGAGTGAAGTGAATGAGATCTTTATGAG 984
Qy 1306 AAACAAATTCAGAGGCGAGAGAAATCTTTGATGAGTCAAGAGAAAGGTGTACAGAACTG 1365
Db 985 AAACAAATTCAGAGGCGAGAGAAAGTCTTTGATGAGGAGAAATGAGGTGTACAGAAATG 1044
Qy 1366 GACTCTGCTAGTATGAGCTGTGTGTTAACAGGCGCTGTGTGTAATGCGAAGATTTGAC 1425
Db 1045 AGCTCAGCTATATATTTCCCTGTATGAGCAATCTTTGCTGTGTACCCGAAATTAAGT 1104
Qy 1426 GAGATGAGGCAACGACTACAACTTCAACAGAGAGGCTTATGTTAGCAAGCCAAAG 1485
Db 1105 GAGATGAGGCAACGACTACAACTTCAACAAAGAGAGATATGAGCAAAATCAAAAG 1164
Qy 1486 AAGCTTCTACCTTGCCCATTTGCTTATGCAAAATCTCTTGCCCGCTTAATAGAACTTCC 1545
Db 1165 AAGTGTATTTGATTAACCTATTTGCAATGCAAAATCTCTTGCCCGCTTAATAGAACTGCC 1224
Qy 1546 TCTCCACTAGCAAA 1559
Db 1225 TCTCTTCAAGATA 1238

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RESULT 4 US-10-401-321-75

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; Sequence 75, Application US/10401321
; Publication No. US2003023679A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kilshore, Ganesh M.
; APPLICANT: Ellich, Tedd D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula

```

```

; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherri J.
; APPLICANT: Baerson, Scott R.
; TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
; FILE REFERENCE: 11899.0216.DVUS01 (MOBT:216--1)
; CURRENT APPLICATION NUMBER: US/10/401,321
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-401-321-75

```

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Query Match 46.7%; Score 806.4; DB 12; Length 1239;
Best Local Similarity 83.5%; Pred. No. 3.7e-219;
Matches 914; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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Qy 466 GGTGATCAAGAACTGMAAGAGAGCACTTCTGTACAGTCCAGTTGTGTGCTAGC 525
Db 145 GGTGMAAGCAATCTATATATGACGGAATTTTCTGTACGCTGTCTATTTGGCTACT 204
Qy 526 CCAAGTGAAGAAATGACTGTGTCAACAGAAAAAGGTATATGTGTATTAAAGAG 585
Db 205 CCAATCTGAGAACGACGATGACATCGAACAGATGTCTATGATGTGTTGAGGAG 264
Qy 586 GCAGCTTATGAAAGGCGAGCTGATCTACCGATGATTTAGAGTGAACCGGATAT 645
Db 265 GCAGCTTGTGAAAGGCGAGCTGATCTACCAATGATTTAGAAAGTGAACCGGATATA 324
Qy 646 GTTGTTCAGAGAAATTTGGCTTTGAGTGAAGCAATGATGTTGTGCGAATATGT 705
Db 325 CCAATTCGGGGAATTTGGCTTTGAGTGAAGCAATGATGTTGTGTTGAGTATGT 384
Qy 706 GCAGATATCAAAAGACATTTTACTTGAAGCAAGCTAATGACCCAGAGAGAGAGA 765
Db 385 GCAGATATCAAAAGACATTTTACTTGAAGCAATGATGTTGTGTTGAGTATGT 444
Qy 766 GCTATCTGGGCAATATATGTGTGTGTGCGAGGAAACGATGAGCTTTGATGGCCCTAAT 825
Db 445 GCTATCTGGGCAATATATGTGTGTGTGCGAGGAAACGATGAGCTTTGATGGCCCAAC 504
Qy 826 GCATCCCACTAACTCCGCAAGCTTTAGATAGTGGAGACCAAGCTGGAAGATATTTTTC 885
Db 505 GCATCAATATATTAACCCCGAGGCTAGATAGTGGGAAAAATGGCTGAGAAAGTGTTC 564
Qy 886 AGTGGGCGGCAATTTGATATGCTTATGCTGCTTTATCCGATCTGTCCAGATTTCT 945
Db 565 AATGGGCGGCAATTTGATGATGCTGCTGCTGCTTTGTCCGATCAAGTTTCAACTTTC 624
Qy 946 GTTGATATTCAGCCATTCAGAGATATGATTTGAGAGAAATGAGTGAAGCTTTGGAATCC 1005
Db 625 GTTGATATTCAGCCATTCAGAGATATGATTTGAGAGAAATGAGTGAAGCTTTGGAATCC 684
Qy 1006 AGATACAAAACCTTCGATGAGCTATATCTATTGTTACATATGTTGCTGTGACTGTAGGA 1065
Db 685 AGATACAAAACCTTCGAGCACTATACCTTTATTTGTTATATGTTGTGTGTAAGTGG 744
Qy 1066 TTGATGAGTGTTCAGATTATGAGTATGCACTGGAATCAAGGCAACAGAGAGTGT 1125
Db 745 TTGATGAGTGTTCAGATTATGAGTATGCCCCGTGAATCAAGGCAACAGAGAGGCT 804
Qy 1126 TATATATGCTGCTTTGGCTTTTAAAGGCTTGCAATCAACTAACCAATATATCTAGAGATGA 1185
Db 805 TATATATGCTGCTTTGGCTTGAGGAGTCCAAATCAATTAACATACATCTCAAGAGATGT 864
Qy 1186 GGAAGAGTCCAGAGAGAGAGAGATATCTTGTCTCAAGATGAATTAGACAGGAGAGG 1245
Db 865 GGAAGAGTCCAGAGAGAGAGAGATCTTGTCTCAAGATGAATTAGACAGGAGAGG 924
Qy 1246 CTCTCCGACGAAACATATTTGCTGGAAGAGTGAAGTGAAGTGAAGGAACTTTATGAG 1305

```

Db	925	CTATCCGATGAAGATATATTGTCTGSAAGGGGTGACCCGATTAATGAGAAATCTTTATGAAG	984
Qy	1306	AAACAATTTTCAGAGGGGAGGAATTTCTTTGTAATAGTCAGAGAAAGGTGTCACAGAACTG	1365
Db	985	AAACAAATACATAGGGCAAGAAAGTTCTTTTATAGAGGAGAAATAGGGGTGACAGAAATTG	1044
Qy	1366	GACTCTGCTAGTAGATGGCCCTGTGTAAACAGCGCTGCTGTGTATGCGCAAGATATTGGAC	1425
Db	1045	AGCTCAGTAGTAATATTTCCCTGTATGGGCATCTTTGCTCTGTACCGCAAAATACTAGAT	1104
Qy	1426	GAGATTGAAGCCACGACTACACAACATTCACAGAGGGGCTTATGTTAGAACCCAAAG	1485
Db	1105	GAGATTGAAGCCATGACTACACACACTTCACAAAGAGAGATATGAGAGAAATTCAAAG	1164
Qy	1486	AAGCTTTCACCTTGGCCCATTTGCTTATGCAAAATCTCTTGTGCCCTTAATAGAACTTCC	1545
Db	1165	AAGTTGATTTGATTACTATTCATATGCATATGCAAAATCTCTTGTGCTCTCCACAAAATCTGCC	1224
Qy	1546	TCTCCACTAGCAAA 1559	
Db	1225	TCTCTTCAAGATA 1238	

```

RESULT 5
US-09-938-842A-729
: Sequence 729, Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Krieps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: TITLE OF INVENTION: SAME, AND METHODS OF USE
: FILE REFERENCE: SCRIPT300-3
: CURRENT APPLICATION NUMBER: US/09/938, 842A
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227,866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 729
: LENGTH: 1269
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
: US-09-938-842A-729

```

Query Match	33.5%	Score 578.4;	DB 10;	Length 1269;
Best Local Similarity	72.5%;	Pred. No. 4.7e-154;		
Matches 766;	Conservative 0;	Mismatches 281;	Indels 9;	Gaps 1

QY	474	AAGAACTGMAAAGGGAGACATYTCCTCTACAGTCAGATTGGTGGCTAGCCCACTGG	533
Db	177	AAGGAACCGAAGTAGAAGATTTGGTGTGTGTCTTAAGCTTAGTACGAAGTCCTCTGG	236
QY	534	AGAAATGACTGTGTCTCATGAGAGAAAAGGTGTATGTATGTGTGATTTAAAGCAGCAGCTTT	593
Db	237	AGAGATAGCTCTTTATCTGAAAGAGAAAGGTTTAAACAATGTGTGTGTAAACAAACCTCTTT	296
QY	594	AGTGAAGAGGCAGCTGAGATCTAC-----CGATGATTTTGAAGTGAGCCGAGATTT	644
Db	297	GGTGAACCAACAGCTTAAGGTCTTTCTTTCTTAATGACCTTGTATGTAAAGAACACACAAGTGT	356
QY	645	TGTTGTTCAGGGAAATTTGGGCTTGTGTGAGTGAAGCATATGATCGTTGTGGCCAGATATG	704
Db	357	TGTTCTTCGTGGAGTTTCAAGTTTGTGTGGGTGAAGCTTATGATCATGGCGTGAAGTTTG	416
QY	705	TGCAGAGTATGGAAGACATTTTACTTAGAAGCAAGCTATATGATACCCCAAGAGAAAG	764
Db	417	CGCTGAATATGTCTAAGACCTTTATCTTATCTGAACTTTGCTATTAGACACCGAAAGGGGAAA	476

OY	765	AGCTATCTGGGCAATATATGTGTGTGACAGAGAAACGATGAGCTGTGTGATGGCCCTAA	824
Db	477	GGGGATTTGGGCATCTACGTTTGGTGTGAGAAAGAACTGATACCTTGTGGATGGGCCAA	536
OY	825	TGCATCCACATPACTCTCGCAAGCTTTAGATAGGTGGGAGCCAGCGTCGAGAGATATTTT	884
Db	537	TGCTTCACATPACTCCCATGAGCTTTTAGATAGAGGAAACAAAGTTAGAGATCTTTT	596
OY	885	CATTGGGCGGCATTTTGATATCTGTAATGCTGCTTATCCGATACTGTCTCCAGATTTCC	944
Db	597	CCGTTGTCGCTTTTGTGATATGCTTGAATGCTGCTCTCGCATACAGTTGTCTAATGCC	656
OY	945	TGTTGATATTCAGCCCATTCAGAGATATGATTTGAAGAAATGGGTATGACCTTTGGAATC	1000
Db	657	GGTCGATATTCACCCATTTCGAGACATGATCGAGAGAAATGGAATGCACTTTGAAGAAATC	716
OY	1005	CAGATACAAAACCTTCGATGACCTATATCTATTTGTAATGTTCTGTGACTGTAGG	1060
Db	717	GAGATACCAAGAACTTGATGATCTATPACTTATCTGTAATGCTGTGAAACGTCGG	776
OY	1065	ATTGATGAGTGTCCAGATTATGGGTATTCACCTGATCAAGGCAACACAGAGATGT	1122
Db	777	ATTGATGACGCTTCGGGTATGGGAATGATCTTAAGTCGAAACCAACCGAAGATGT	836
OY	1125	ATATATATGCGTCTTTGGCTTTAGGGCTTCGAAATCAATCAATPACTCAGAGATGT	1180
Db	837	TTTCAACGCTGCTTGTGGCTTTGGTATATGCCATATAGCTTATCTPACTACTCAGAGCGT	896
OY	1185	AGGAGAGAATGCGCAGAGAGAGAAAGATATCTTGTGCTTCAGAGTAATGACACAGCGAGG	1242
Db	897	AGCGAAGATCGAGAGAGAGAAAGGTTTATCTGCTCAGAGTGAATTTGGCTCAGCGCTGG	956
OY	1245	GCTCTCCGACGAAGACATATTTTGTGTGAAAGATGACTGATATGTGAGAGAACTTTATGAA	1300
Db	957	TCTTTCAAGATGAAGACATATTCGCCGAAAAGTAACTGATAAATGGAGAAACCTTCATGAA	1010
OY	1305	GAAACAAATTCAGAGGGCGAGGAAATCTCTTTGATGAGTCAAGAGAAAGGTGCAAGAACT	1360
Db	1017	AATGCAAGCTTAAACGACGACAGATGTTCTTTGACGAACTGAGAAAGCGTCACCGAGCT	1070
OY	1365	GGACTCTGTAGTATGATGGCTGTGTATTAACAGCGCTGTTGTGTATCGCAAGATATTGGA	1422
Db	1077	CAGTCCGCTAGAGATGGCTGTATGGGCTTCAATGCTATGTATGACGAGAAATACGTGA	1130
OY	1425	CGAGATTGAAGCAACGACTACACAACTTCACAAAGAGGCTTATGTTAGCAAGCCAA	1480
Db	1137	CGAGATTGAAGGAAATGATTAACAAATTTTACTPAAGAGAGCTTATGTGGGAGAAATCAA	1190
OY	1485	GAAGCTTCTACCTTGGCCATGCTTATGCAAAATC	1520
Db	1197	GAAATTTGACGCTTTGCAATGGCTTATGCTPAATC	1232

```

RESULT 6
US-10-149-759-53
; Sequence 53, Application US/10149759
; Publication No. US20030157592A1
; GENERAL INFORMATION:
; APPLICANT: Lerchl, Jens
; APPLICANT: Renz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reindl, Andreas
; APPLICANT: Cirpus, Petra
; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins
; TITLE OF INVENTION: Involved in the synthesis of tocopherols and
; FILE REFERENCE: BASE/NAE 133/99 PCT/US
; CURRENT APPLICATION NUMBER: US/10/149,759
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: PCT/EP/00/12698
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 82

```

SOFTWARE: WordPerfect version 6.1
 SEQ ID NO 53
 LENGTH: 684
 TYPE: DNA
 ORGANISM: Physcomitrella patens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (2)..(397)
 OTHER INFORMATION: 02_pprocl_046_a07rev
 US-10-149-759-53

Query Match 10.3%; Score 177.4; DB 13; Length 684;
 Best Local Similarity 68.0%; Pred. No. 9.5e-40;
 Matches 247; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1171 ATACTGAGATGTAGAGAGATGCCAGAGAGAGATATCTTCCCTCAAGATGAA 1230
 DB 5 ATCCAGAGAGATGTAGAGAGATGACGCCGTGACAGATATCTCCACAGAGTAA 64
 QY 1231 TTACACAGAGAGAGGCTCTCCGACGACATATTTGCTGGAAGAGTACTGATAGTG 1290
 DB 65 CTGGACAGCTTTCGGCTCTCGATGACACATTTTGTGCGAAAAGTTACTGATTAATG 124
 QY 1291 AGGAATTTATGAGAAACAAATTCAGAGGCGAGAAATTTCTTGATGACTCAGAGAA 1350
 DB 125 AGGCATATCATGAAAGACCAATTAAGAGCTAGAGTGTCTTTGTGAGGCTGAGAAA 184
 QY 1351 GGTGTACAGAACTGAGCTGTAGTATGAGGCTGTGTATGACAGCGCTGCTGTAT 1410
 DB 185 GGTGTACGTGAGCTGAGAAAGACGTGCTGTGTGTGTGCTGCTTCAATCTTTAC 244
 QY 1411 CGCAGATATTTGAGAGATTTGAGCAAGCACTCAACAATTCACAGAGAGGCTTAT 1470
 DB 245 CAGGAATTCGTGAGAGCCATTTGAGCCAACTTACGATTAATTGACAAAAGAGCTTAC 304
 QY 1471 GTTAGCAAGCCAAAGAGCTTCTACCTTGGCCATTTGCTTATGCAAAATCTTGTGCCC 1530
 DB 305 GTAGCAAGGTGAGAAAGAGCTGCTTCTACCTTATGCGCTTATGAGAGCGTGTGCTCA 364
 QY 1531 CCT 1533
 DB 365 CCT 367

RESULT 7
 US-10-236-508-9
 Sequence 9, Application US/10236508
 Publication No. US20030167512A1
 GENERAL INFORMATION:
 APPLICANT: Monto H. Kumagai
 APPLICANT: Guy R. della-Cioppa
 APPLICANT: Robert L. Erwin
 APPLICANT: David R. McGee
 TITLE OF INVENTION: METHOD OF DETERMINING THE PRESENCE OF A TRAIT IN A PLANT BY
 TITLE OF INVENTION: TRANSFECTING A NUCLEIC ACID SEQUENCE OF A DONOR PLANT INTO A
 FILE REFERENCE: 008010137US05
 CURRENT APPLICATION NUMBER: US/10/236,508
 CURRENT FILING DATE: 2002-09-06
 NUMBER OF SEQ ID NOS: 48
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 9
 LENGTH: 114
 TYPE: DNA
 ORGANISM: Tomato mosaic virus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (28)...(114)
 US-10-236-508-9

Query Match 3.0%; Score 52.4; DB 13; Length 114;
 Best Local Similarity 79.8%; Pred. No. 0.00015;
 Matches 75; Conservative 0; Mismatches 16; Indels 3; Gaps 1;

QY 245 TGACATGCTGTGCTTTGTGTGTGAGTTTCTCCACTTCGAGCTTCGAATGGA 304
 DB 23 TAAATATGCTGTGCTTGTGTGTGTGAGTTTCTC---CTTGACGTCTCAATGGA 79
 QY 305 CAGATTTGATTCAGTCCGAGAGAAACCG 338
 DB 80 CAAGTTTCATGATCAGTCCGAGAGAAACCG 113

RESULT 8

US-10-103-450-12
 Sequence 12, Application US/10103450
 Publication No. US20030219897A9
 GENERAL INFORMATION:
 APPLICANT: KUMAGAI, MONTU H.
 APPLICANT: DELLA-CIOPPA, GUY R.
 APPLICANT: DONSON, JONATHAN
 APPLICANT: HARVEY, DAMON A.
 APPLICANT: GRILL, LAURENCE K.
 TITLE OF INVENTION: THE CYTOPLASMIC INHIBITION OF GENE
 TITLE OF INVENTION: EXPRESSION BY VIRAL RNA
 FILE REFERENCE: 008010086US02
 CURRENT APPLICATION NUMBER: US/10/103,450
 CURRENT FILING DATE: 2002-03-20
 PRIOR APPLICATION NUMBER: 09/436,068
 PRIOR FILING DATE: 1999-11-08
 PRIOR APPLICATION NUMBER: 08/260,546
 PRIOR FILING DATE: 1994-06-16
 PRIOR APPLICATION NUMBER: 08/184,237
 PRIOR FILING DATE: 1994-01-19
 PRIOR APPLICATION NUMBER: 07/923,692
 PRIOR FILING DATE: 1992-07-31
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 12
 LENGTH: 114
 TYPE: DNA
 ORGANISM: Tomato mosaic virus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (28)...(114)
 US-10-103-450-12

Query Match 3.0%; Score 52.4; DB 13; Length 114;
 Best Local Similarity 79.8%; Pred. No. 0.00015;
 Matches 75; Conservative 0; Mismatches 16; Indels 3; Gaps 1;

QY 245 TGACATGCTGTGCTTTGTGTGTGAGTTTCTCCACTTCGAGCTTCGAATGGA 304
 DB 23 TAAATATGCTGTGCTTGTGTGTGTGAGTTTCTC---CTTGACGTCTCAATGGA 79
 QY 305 CAGATTTGATTCAGTCCGAGAGAAACCG 338
 DB 80 CAAGTTTCATGATCAGTCCGAGAGAAACCG 113

RESULT 9

US-10-103-450-12
 Sequence 12, Application US/10103450
 Publication No. US20020155605A1
 GENERAL INFORMATION:
 APPLICANT: KUMAGAI, MONTU H.
 APPLICANT: DELLA-CIOPPA, GUY R.
 APPLICANT: DONSON, JONATHAN
 APPLICANT: HARVEY, DAMON A.
 APPLICANT: GRILL, LAURENCE K.
 TITLE OF INVENTION: THE CYTOPLASMIC INHIBITION OF GENE
 TITLE OF INVENTION: EXPRESSION BY VIRAL RNA
 FILE REFERENCE: 008010086US02
 CURRENT APPLICATION NUMBER: US/10/103,450
 CURRENT FILING DATE: 2002-03-20
 PRIOR APPLICATION NUMBER: 09/436,068

	Best Local Similarity	49.0%;	Pred. No. 0.31;	Matches 144;	Conservative 0;	Mismatches 147;	Indels 3;	Gaps 1;
QY	962	TCAGAGATATGATTTGAAGAAATGCGTATGACCTTGTGAAAAATCCAGATACAAAATTTCG	1021					
Db	347	TCGACGAACCTGATCGACCGCGCTCTCCATGACGAGCTGCGCGGAGACCTACAGACCTGGG	406					
QY	1222	ATGAGCTATATCTCAATGTTATCTATGTTGCGTGCATGTTGAGATTTAGTAGTGTTCAG	1081					
Db	407	ACGACCTTCAAGGTCTTACTGTCGCGCTGTGTGGCAGGGGCACTGCGCGGCTTCGCTCGGCG	466					
QY	1082	TTATGGGTATTTGCACTGTAATCAAAAGGCAACAAGAGAGTGTATATATATGCTGCTTGG	1141					
Db	467	TGTTTCGGACGGAACCGGCGCGCGCG---GGCGGAGCGGCGGTCAAGTATCGCGACA	523					
QY	1142	CTTTAGGGCTTGGCAATCACTTAACCAATATATCTGAGATGTGAGAGAAAGTCCAGAA	1201					
Db	524	CCCTCGGCGCTCGCTCTCCAGCTTCACCAACATCTCCGAGATGACGACAGACGCGCGAG	583					
QY	1202	GAGAGAGATATACCTTGGCTGCAAGATGAAATTAAGACACAGGAGGCGTCCGACG	1255					
Db	584	GCGGCGGACCTATCTGCCCCGCGCAGCACTTGGCCAAATTTGGCGTCTCGGCGG	637					

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RESULT 13
US-10-156-761-1/C
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OR INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

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	Query Match	2.5% Best Local Similarity	Score 42.8	DB 15	Length 9025608
	Matches 144	Conservative 0	Mismatches 147	Indels 3	Gaps 1
QY	962	TCAGAGATATGATTGAGAGAAATGCGTATGACCTGTGTGAAATCCAGATACAAAATTTCG	1021		
Db	2025601	TCGACGAACCTATGACCGCGCTCTCCATGACGTCGCGGAGACCTTACGAGACCTTCGG	20255422		
QY	1022	ATGAGCTATATCTGATTTACTATGTTGCTGTGACTGTAGATTTGATGATCTTTCAC	1081		
Db	2025541	ACGACCTTAAGGTCTACTGCGCGTGTGTGGCAGGGGCATCGCGCGCGTCTCGCTCGGCG	20254822		
QY	1082	TTATGGGATTTGCACTGCAATCAAAAGCAACAAGAGATGATATATATCTCTTCG	1141		
Db	2025481	TGTTCCGACAGGAACCGGCGCCGCGC---GCGCGAGCGCGCTCAAGTACGTCGACA	20254255		
QY	1142	CTTTAGGCGCTTGCAATCACTTAACCAATATATCTCAGATGTGAGAGAGATGCCAGAA	1201		

Db 2025424 CCCCTGGGCTTCGCTCTCCAGTACCAACAATCTCTCCGGGAGCTACGGGAGGAGCGCCAGG 2025355

Gy 1202 GAGGAAGAGTACTTGGCTCAAGATGAATTTAGACAGGAGGCTTCCGAGC 1255

Db 2025364 GCGGCGGCACTATCTGCGCGGACGACGACTCGGCAATTTGCGTCTCGGCGC 2025311

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RESULT 14
US-10-312-841-2
: Sequence 2, Application US/10312841
: Publication No. US20030186277A1
: GENERAL INFORMATION:
: APPLICANT: Epigenomics AG
: TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
: FILE REFERENCE: E01/1208/WO
: CURRENT APPLICATION NUMBER: US/10/312,841
: CURRENT FILING DATE: 2002-12-30
: NUMBER OF SEQ ID NOS: 2
: SEQ ID NO 2
: LENGTH: 3673778
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (379615)
: US-10-312-841-2

```

	Query Match Best Local Similarity	2.4% 46.3%	Score No.1,6 Pred. No.1,3e+02	DB 13	Length 363778	Matches 137	Conservative 0	Mismatches 159	Indels 0	Gaps 0
QY	24	TTTTGCTCTTTGTGATGAGTGCATTTCCCTCTCTCTGTGTGAAGCGAAAGTCGTTCACT	83							
Db	2288581	TTTTGTTTGTAGTTTTTAAAGTAGTGGGATTATAGGTGTATTATTTAAAGTTGGTTAAT	2288640							
QY	84	TTCTTATATCCGATTTTATATATGTTGAATTAAGTGATAGACTAGTGGATATCTAC	143							
Db	2288641	TTTTGTATTTTGTAGTAGAGACGGGGTTTATTTATAGTTGGTTAGGTTATTTAAATTTT	2288700							
QY	144	AAGTATTGGTTTTTGTATATAATATAGCTGAGGTGAGAAAGTAACTAAAGAAAGACAA	203							
Db	2288701	AATTTTAAAGGATTTGTTTTTATTTTGGTTTTTAAAGTTGGATTAAGGTGTGTAAT	2288760							
QY	204	AACATGGAATTTGTTTATAGACACCGAGTTTCTGTTTCATGAGCATGTCTGTGCTTT	263							
Db	2288761	GTAATCGGTTTGATTGAGGTTTATATATTTGATGTTTTCGGGGGTTTGGTGTTTTTT	2288820							
QY	264	GTGTGGGTTGTTTCTCCCACTTCCAGAGTCTCGAATGGACAGATTTGTTCATT	319							
Db	2288821	TTTTTTAATTTTTTTTTTGGGTTGGGTTGTTTATATGTAGTGGTTTGTAAGTTT	2288876							

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RESULT 15
US-09-736-457-1310/c
; Sequence 1310, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, AiJun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457

```

CURRENT FILING DATE: 2000-12-13
 NUMBER OF SEQ ID NOS: 1864
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 1310
 LENGTH: 534
 TYPE: DNA
 ORGANISM: Homo sapien
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(534)
 OTHER INFORMATION: n = A,T,C or G
 US-09-736-457-1310

Query Match 2.4%; Score 41.2; DB 10; Length 534;
 Best Local Similarity 57.9%; Pred. No. 0.62;
 Matches 73; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy	97	TTTTTAATCGTTGAAATTAGTGATGACTCTAGTGATATCTACAAAGTATTGGTTT	156
Db	465	TATTTACAAACTTTATCAATAGTAAATCTAAATGTAATAATTAATCTATGATTTT	406
Qy	157	TTGATAAATAGGCTGAGGTGAGGTACATAAAGAGCAAAACTTGGGAATTG	216
Db	406	ATACAAATACTCTAAAGTACAAATGTAAATGTTAAATGCTGAATAAACATTTCACCTT	346
Qy	217	TTTTAG 222	
Db	345	TTCCAG 340	

Search completed: January 16, 2004, 06:30:02
 Job time : 1348 secs

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OM nucleic - nucleic search, using sw model

Run on: January 16, 2004, 00:54:54 ; Search time 3744 Seconds
(without alignments)
11217.451 Million cell updates/sec

Title: US-09-847-081b-1
Perfect score: 1728
Sequence: 1 agaaaccagaagaagaac.....tcatcaaacctcaagtgg 1728

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estcov:*
6: em_estcpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
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17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
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21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	655.4	37.9	781	13	B0511016 EST18431
2	621.6	36.0	751	12	B0046203 EST195321
3	605.2	35.0	787	12	BM410846 EST185173
4	568.4	32.9	677	10	BG351357 104A12 Ma

Result No.	Score	Query Match	Length	ID	Description
5	552.2	32.0	686	9	AW442101 EST311497
6	551.2	31.9	765	12	BM408984 EST185311
7	541.2	31.3	682	12	BM409200 EST185357
8	532.8	30.8	672	9	AW442407 EST311803
9	532.2	30.2	642	10	BE433198 EST319727
10	515.8	29.8	676	9	AW222027 EST298838
11	498.2	28.8	634	12	BM412533 EST186860
12	487.2	28.2	599	12	B1921390 EST414293
13	486.4	28.1	600	10	BE460889 EST412308
14	483.4	28.0	623	10	BE432511 EST399040
15	478.8	27.7	685	9	AW221932 EST298743
16	474.4	27.4	819	13	B0636463 EST300127
17	473.2	27.4	582	9	AW223316 EST300127
18	466.8	27.0	582	9	AW223666 EST300477
19	466.4	27.0	581	10	BE432955 EST399484
20	466.4	27.0	623	12	BM536249 EST1869271
21	461.4	26.7	791	9	AW223528 EST300339
22	458.4	26.5	573	10	BE433508 EST406386
23	458.4	26.5	605	9	BE435064 EST406142
24	458.2	26.5	585	9	AW222245 EST299056
25	458	26.5	1655	11	AY11032 Zea mays
26	457.8	26.5	565	10	BE432595 EST399124
27	453.2	26.2	562	10	BE433966 EST405044
28	449.4	26.0	581	9	AW222806 EST299617
29	442.4	25.6	556	9	AW222152 EST298963
30	439.6	25.4	542	10	BE431550 EST36365
31	439	25.4	543	12	BM411875 EST186202
32	437.4	25.3	634	9	AW441216 EST310612
33	435	25.2	555	10	BE460463 EST411882
34	434.4	25.1	566	10	B1112979 EST440662
35	431.6	25.0	542	10	BE432748 EST39277
36	429.2	24.8	563	10	BE461396 EST412815
37	427.8	24.8	580	9	AW092680 EST285870
38	427.6	24.7	563	10	BE437095 EST408213
39	426.8	24.7	536	10	BE434911 EST405989
40	425.4	24.6	558	9	AW222427 EST29238
41	425.4	24.6	1201	11	AY108547 Zea mays
42	424.2	24.5	744	12	BM412719 EST587057
43	423.6	24.5	551	10	BE432084 EST398613
44	415.2	24.0	536	9	AW223238 EST300049
45	409.2	23.7	519	10	BE433537 EST400066

ALIGNMENTS

RESULT 1
B0511016/c
LOCUS
DEFINITION
B0511016
Accession
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
EST.
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
3' end, mRNA sequence.

REFERENCE
AUTHORS
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
Karimychewa, S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished
On Jun 10, 2002 this sequence version replaced gi:21369885.
Other ESTs: EST618430

TITLE
JOURNAL
COMMENT
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics

[illegible]

Db

	Query Match	Best Local Similarity	Score 621.6;	DB 12;	Length 751;
	Matches 690;	Conservative 0;	Mismatch 59;	Indels 3;	Gaps 3
Qy	438	AAATGCGATCCAGGATTTATCTCTGGGCGATCCAGAACTGAAAAAGGAGACATT			
Db	1	AAATGCGATTGAGATATTCGTGTTTAAAGAGATCAAGAACTGAAATGGAAGAGATT			
Qy	498	CTCTGTACAGTCGAGTTGGTGGCGTAGCCGACGTGGAGAAATGACTGTATCAGAGAA			
Db	61	TTCTGTACAGTCGAGTTGGTGGCTAGTCGACGTGGAGAAATGCGTGTGTATCAGAGAA			

QY 558 AAAGTGTATGATGTGTATTAAGCAGGACCTTAGTGAAGGACGCTGAGATCTAC 617
 DB 121 AAAGTGTATGATGTGTATTAAGCAGGACCTTAGTGAAGGACGCTGAGATCTAC 180
 QY 618 CGATGATTTAGAGGAGGACCGGATTTGTTCCAGGAAATTTGGCTTTGTAAGCA 677
 DB 181 TGAGACATAGAGGAGGACCGGATTTGTTCCAGGAAATTTGGCTTTGTAAGCA 240
 QY 678 AGCATATGATGTGTGTGGGAGATATGTGACAGATATGCAAGACATTTACTTGAAC 737
 DB 241 AGCATATGATGTGTGTGGGAGATATGTGACAGATATGCAAGACATTTACTTGAAC 300
 QY 738 CAAGTAAATGACCCAG 797
 DB 301 CATGCTAATGATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 QY 798 AAGGATGAGCTTTGTTGATGATGATGATGATGATGATGATGATGATGATGATG 857
 DB 361 AAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 QY 858 GTGGAGAGCAGGCTGGAAGATATTTTCAGTGGGCGCCATTTGATGATGATGATG 917
 DB 421 GTGGAGAGCAGGCTGGAAGATATTTTCAGTGGGCGCCATTTGATGATGATGATG 480
 QY 918 TTTATCCGATATCTGCTCCAGATTTCTGTTGATATTTAGCCATTCAGAGATATG 977
 DB 481 TTTATCCGATATCTGCTCCAGATTTCTGTTGATATTTAGCCATTCAGAGATATG 540
 QY 978 AGGAATGCGATGAGACTGTGTGAAATCCAGATACAAACTTTGATGATGATGATG 1037
 DB 541 AGGAATGCGATGAGACTGTGTGAAATCCAGATACAAACTTTGATGATGATGATG 600
 QY 1038 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1096
 DB 601 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
 QY 1097 CTGAATCAAGGCAACAAGAGAGATGATATATATGCTGC-TTTGGCTTTAGGCTTGA 1155
 DB 661 CTGAATCAAGGCAACAAGAGAGATGATATATATGCTGC-TTTGGCTTTAGGCTTGA 720
 QY 1156 AATCACTTACCAATATATCTCAGAGATGAGG 1187
 DB 721 AATCACTTACCAATATATCTCAGAGATGAGG 751
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 LOCUS BM410846 787 bp mRNA linear EST 22-JAN-2002
 DEFINITION EST585173 tomato breaker fruit Lycopersicon esculentum cDNA clone
 C18G54F18 5' end, mRNA sequence.
 ACCESSION BM410846
 VERSION BM410846.1 GI:18262476
 KEYWORDS EST.
 ORGANISM Lycopersicon esculentum (tomato)
 SOURCE Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 787)
 Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai,
 J., Bougri, O., Kirkness, E., Uteback, T., Van Aken, S., Roming,
 C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
 Generation of ESTs from tomato fruit tissue, breaker stage (2002)
 Unpublished
 TITLE
 JOURNAL
 COMMENT
 Contact: CUGI
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 This clone is available through the Clemson University Genomics
 Institute
 Seq primer: T3.

FEATURES
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 Location/Qualifiers
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 /lab_host="SOLR"
 /clone_lib="tomato breaker fruit"
 /note="vector: pBluescriptSMC4dupc; Site 1: EcoRI;
 Site 2: XhoI; supplier: Boyce Thompson Institute;
 sequencing: The Institute for Genomic Research.
 Fruit were harvested at the breaker stage (first sign of
 lycopene accumulation on the blossom end of fruit). Fruit
 were cut in half and the seeds and locules were discarded
 prior to freezing the pericarp."
 BASE COUNT 230 a 132 c 211 g 214 t
 ORIGIN
 Query Match 35.0%; Score 605.2; DB 12; Length 787;
 Best Local Similarity 85.6%; Pred. No. 5e-140;
 Matches 673; Conservative 0; Mismatches 113; Indels 0; Gaps 0;
 QY 491 GCATTTCTGTGACAGTCCAGTTGGTGGCTAGCCCGCTGAGAAATGACTGTGCAT 550
 DB 2 GGAAATTTCTGTAGCGTCTGCTATTTGGCTACTCCACTGAGAGACGAGATGACAT 61
 QY 551 CAGAGAAAAGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 610
 DB 62 CGAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 121
 QY 611 GATCTACCGATGATTTAGAAATGAAAGCGGATATTTGTTCCAGGAAATTTGGCTTGT 670
 DB 122 GATCTACCAATGATTTAGAAATGAAAGCGGATATTTGTTCCAGGAAATTTGGCTTGT 181
 QY 671 TGAGTGAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 730
 DB 182 TGAGTGAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 241
 QY 731 TAGGAACCAAGCTAATGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 790
 DB 242 TAGGAACCAAGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 301
 QY 791 GCAGAGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 850
 DB 302 GCAGAGAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 361
 QY 851 TAGATAGGTGGAGACCGAGCTGAGAGATTTTTCAGTGGGCGCCATTTGATATGCTTG 910
 DB 362 TAGATAGGTGGAGAAATAGGCTAGAGAGATTTTTCAGTGGGCGCCATTTGATATGCTTG 421
 QY 911 ATGCTGCTTTATCCGATATCTGCTCCAGATTTCTGTTGATATTTAGCCATTCAGAGATA 970
 DB 422 ATGCTGCTTTATCCGATATCTGCTCCAGATTTCTGTTGATATTTAGCCATTCAGAGATA 481
 QY 971 TGATTTGAAGAGATGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1030
 DB 482 TGATTTGAAGAGATGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 541
 QY 1031 ATCTCTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1090
 DB 542 ACCTTTATTTGATTTATTTATTTGCTGTGATGATGATGATGATGATGATGATGATG 601
 QY 1091 TTGCACTGAATCAAGGCAACAAGAGAGATGATATATGCTGCTTTGGCTTTAGGCGC 1150
 DB 602 TCGCCCTGATCAAGGCAACAAGAGAGATGATATATATGCTGCTTTGGCTTTAGGCGC 661
 QY 1151 TTGCAATCACTAATCAATATCTCAGAGATGATGATGATGATGATGATGATGATGATG 1210
 DB 662 TCGCAATCAATTAATCAATATCTCAGAGATGATGATGATGATGATGATGATGATGATG 721

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Qy 1211 TATACCTGCCCTCAAGATGAATAGACAGGAGGCTCTCCGACGAACATATTTGCTG 1270
Db 722 TCTACTTGCCCTCAGATGAATTAGACAGGAGGCTCTCCGATGAAGATATTTGCTG 781
Qy 1271 GAAGAG 1276
Db 782 GAAGGG 787

RESULT 4
LOCUS BG351357 677 bp mRNA linear EST 11-SEP-2002
DEFINITION 104A12 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA
sequence.
ACCESSION BG351357
VERSION BG351357.1 GI:13180099
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 677)
Crookshanks, M., Emmersen, U., Welinder, K.G. and Nielsen, K.L.
The potato tuber transcriptome: analysis of 6077 expressed sequence
tags
FEBS Lett. 506 (2), 123-126 (2001)
JOURNAL MEDLINE 21475600
PUBMED 11591384
COMMENT Contact: Karen G. Welinder
Institute for Biotechnology
Aalborg Universitet
Sohnegaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358457
Fax: +45 98141808
Email: kgw@bio.auc.dk
Sequenced from the 5' end.
High quality sequence stop: 677
POLYA=No.

FEATURES
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/mol_type="mRNA"
/cultivar="Field grown Kuraz"
/db_xref="taxon:4113"
/tissue_type="tuber"
/clone_lib="Mature tuber lambda ZAP"
/notes="Vector: Lambda ZAP"

BASE COUNT 192 a 102 c 198 g 185 t
ORIGIN
Query Match 32.9%; Score 568.4; DB 10; Length 677;
Best Local Similarity 90.9%; Pred. No. 7.4e-131;
Matches 616; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

Qy 316 GATTCAAGCCGAGAGAAACCGCGCTTTGTATCATCCAGATTCCTGCTGAGATAGG 375
Db 1 GATTCAAGCCGAGAGAAACCGCGCTTTGTATCATCCAGATTCCTGCTGAGATAGG 59
Qy 376 AATTGATGTGAATGGAGATCAAGAAAGGTGGAGACAAAGCTGGAATTTGGCTCT 435
Db 60 AATTGATGTGAATGGAGATTCAGAAAGGTGGAGACAGAGTGAATTTGGGCTT 119
Qy 436 TTAATGTGTATCCAAAGATATTCATGCTTGGGTGATCAAGACTGAAAAGGAGCACT 495
Db 120 TTAATGTGAATTTGAGATATTCGTGTTAGAAAGATCAAGAACTGAGAAATGGAAGGAT 179
Qy 496 TTCTCTGACAGTCAGTTTGGTGGCTAGCCAGCTGAGAAATGACTGTGCATCAGAG 555
Db 180 TTCTCTGACAGTCAGTTTGGTGGCTAGCTGAGAAATGCTGTGTGCATCAGAG 239
Qy 556 AAAAGGTGTATGTGTGTATTAAGCAGGCGAGCTTTAGTGAAGGCGAGCTGAGATCT 615

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Db 240 AAAAGGTGTATGAGTGTATTAAGCAGGCGAGCTTTAGTGAAGGCGATCTGATCT 299
Qy 616 ACCGATATTAGAGAGGAGCCGATATTTGTTCCAGGAAATTTGGCTTGTAGT 675
Db 300 ACTGAGACATAGAGAGGAGCCGATATTTGTTCCGAGTATTTGGCTTGTAGT 359
Qy 676 GAAGCATATGATCGTTGTGGCGAAGTATGTGACAGATATGCAAAAGCATTTTACTTGA 735
Db 360 GAAGCATATGATCGTTGTGGCGAAGTATGTGACAGATATGCTAAAGCATTTTACTTGA 419
Qy 736 ACCAAGTATGACCCCAAGAGAGAAAGAGCATATCTGGGCATATATGTGTGTGAGG 795
Db 420 ACCATGTGTAATGATCTCAGACAGAAAGAGCATATCTGGGCATATATGTGTGTGAGG 479
Qy 796 AGAAGCATGAGCTTGTGTATGAGCCCTAATGATCCACATTAATCCGCAAGCTTTAGAT 855
Db 480 AGAAGCATGAGCTTGTGTATGAGCCCTAATGATCCACATTAATCCGCAAGCTTTAGAT 539
Qy 856 AGGTGGAGACCAAGCTGGAAGATATTTTCAGTGGGGCGGCATTTGATATGCTGATGCT 915
Db 540 AGGTGGAGACCAAGCTGGAAGATATTTTCAGTGGGGCGGCATTTGATATGCTGATGCA 599
Qy 916 GCTTATCCGATACTGCTCCAGATTTCTGTTGATATTCAGCATTCAGAGATATGAT 975
Db 600 GCTTATCCGATACTGCTCCAAATTCCTGTGATATTCAGCATTCAGAGATATGAT 659
Qy 976 GAAGCAATGGCTATGAGC 993
Db 660 GAAGCAATGGCTATGAGC 677

RESULT 5
AM442101 686 bp mRNA linear EST 18-MAY-2001
LOCUS EST311497 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
DEFINITION
AM442101
AM442101.1 GI:6977352
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Lycopersicon esculentum (tomato)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 686)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F.,
Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M.,
Frieser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato fruit tissue
Unpublished
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.

FEATURES
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/clone_lib="tomato fruit red ripe, TAMU"
/notes="Vector: pBluescript SK(-); Site 1: Scori; Site 2:
XhoI; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were

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discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

BASE COUNT 204 a 114 c 182 g 186 t

ORIGIN

Query Match 32.0%; Score 552.2; DB 9; Length 686;
Best Local Similarity 87.9%; Pred. No. 8.3e-127;
Matches 602; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 565 TATGATGTGTATTTAAAGCAGCGCTTTAGTGAAGAGCGAGCTGAGATCTACCGATGAT 624
DB 2 TATGATGTGTATTTAGGCGAGCGCTTTAGTGAAGAGCGAGCTGAGATCTACCGATGAT 61
QY 625 TTGAAGTGAAGCGCGATATTTGTTTCAGGGAATTTGGCTTTGTTAGTGAAGCATAT 684
DB 62 TTGAAGTGAAGCGCGATATTTGTTTCAGGGAATTTGGCTTTGTTAGTGAAGCATAT 121
QY 685 GATCGTTGTGGCGAAGTGTGTGAGAGTATGCAAGACATTTTACCTTAGAACCAAGCTA 744
DB 122 GATAGGTGTGTGAGTGTGTGAGAGTATGCAAGACATTTTACCTTAGAACCAAGCTA 181
QY 745 ATAGCCCGAGAGAGAGAGAGAGTATCTGGGCAATATATGTGTGTGAGAGAGAGAGAT 804
DB 182 ATAGCTCCGAGAGAGAGAGAGAGTATCTGGGCAATATATGTGTGTGAGAGAGAGAT 241
QY 805 GAGCTTTGTGATGCGCTTAATGATCCGACATTAATCTCCGAGAGCTTTAGTGAAGTGAAG 864
DB 242 GAGCTTTGTGATGCGCGCAAGCATATATATTAACCGGAGAGCTTTAGTGAAGTGAAG 301
QY 865 ACCAGGCTGGAAGATATTTTCACTGAGGCGCGCATTTGATATGCTGATGCTGCTTAATCC 924
DB 302 AATAGGCTGGAAGATATTTTCACTGAGGCGCGCATTTGATATGCTGATGCTGCTTAATCC 361
QY 925 GATAGCTGTCCGAGATTTCTGTGTATATCAAGCATTAATGATATGATGAAGAGAT 984
DB 362 GATAGCTGTCTAATCTTCACTGATGATTAATCAAGCATTAATGATGAAGAGAT 421
QY 985 CGTATGAGCTTTGGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1044
DB 422 CGTATGAGCTTTGGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 481
QY 1045 TATGTTGCTGTGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1104
DB 482 TATGTTGCTGTGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
QY 1105 AAGGCAACAACAAGAGTGTATATATATGCTTTGCTTTAGGCTTGAAGTGAAGTGAAGTGAAG 1164
DB 542 AAGGCAACAACAAGAGTGTATATATATGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTT 601
QY 1165 ACCAATATATCTAGAGATGTAGAGAGATGCCAGAGAGAGAGATATCTTGGCTTGAAG 1224
DB 602 ACTAATCTATCTAGAGATGTGTGAGAGATGCCAGAGAGAGAGATATCTTGGCTTGAAG 661
QY 1225 GATGAATTAGCAGAGCGAGGCTCT 1249
DB 662 GATGAATTAGCAGAGCGAGGCTCTAT 686

RESULT 6
LOCUS BM408984 765 bp mRNA linear EST 22-JAN-2002
DEFINITION EST563311 tomato breaker fruit Lycopersicon esculentum cDNA clone
ACCESSION BM408984
VERSION BM408984.1 GI:18260614
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Bukharova; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 765)
Alcala,J., Vrebalov,J., White,R., Vision,T., Karameycheva,S.A., Tsai

TITLE
JOURNAL
COMMENT
Unpublished

Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3

FEATURES

source

Location/Qualifiers

1..765

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/culivar="TA496"

/db_xref="taxon:4081"

/clone="CLEG46P23"

/tissue_type="Pericarp"

/dev_stage="breaker"

/lab_host="SOLR"

/clone_lib="tomato breaker fruit"

/note="Vector: pBluescriptSMK2adapt; Site 1: EcorI;
Site 2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."

BASE COUNT 237 a 122 c 202 g 204 t

ORIGIN

Query Match 31.9%; Score 551.2; DB 12; Length 765;
Best Local Similarity 86.1%; Pred. No. 1.5e-126;
Matches 634; Conservative 0; Mismatches 98; Indels 4; Gaps 2;

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QY 685 GATCGTTGTGGCGAAGTGTGTGAGAGTATGCAAGACATTTTACTTAGAACCAAGCTA 744
DB 61 GATAGGTGTGTGAGTGTGTGAGAGTATGCAAGACATTTTACTTAGAACCAAGCTA 120
QY 745 ATGACCCCGAGAGAGAGAGAGTATCTGGGCAATATATGTGTGTGTCAGAGAACGAT 804
DB 121 ATGACCTCCGAGAGAGAGAGAGTATCTGGGCAATATATGTGTGTGTCAGAGAACGAT 180
QY 805 GAGCTTTGTGATGCGCTTAATGATCCGACATTAATGATGATGATGATGATGATGATGATGAT 864
DB 181 GAGCTTTGTGATGCGCGCAAGCATATATATTAACCGGAGCTTTAATATGATGAGAGAT 240
QY 865 ACCAGGCTGGAAGATATTTTCACTGAGGCGCGCATTTGATATGCTGATGCTGCTTAATCC 924
DB 241 AATAGGCTGGAAGATATTTTCACTGAGGCGCGCATTTGATATGCTGATGCTGCTTATCC 300
QY 925 GATCTGTCTCAAGATTTCTGTGTATATCAAGCATTAATGATGATGATGATGATGATGATGAT 984
DB 301 GATCTGTCTCAAGATTTCTGTGTATATCAAGCATTAATGATGATGATGATGATGATGATGAT 360
QY 985 CGTATGAGCTTTGGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1044
DB 361 CGTATGAGCTTTGGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 420
QY 1045 TATGTTGCTGTGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1104
DB 421 TATGTTGCTGTGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 1105 AAGGCAACAACAAGAGTGTATATATATGCTTTGCTTTAGGCTTGAAGTGAAGTGAAGTGAAG 1164
DB 481 AAGGCAACAACAAGAGTGTATATATATGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTT 540

QY 1165 ACCAATATATCTCAGAGATGTAGAGAAATGCCAGAAAGAAAGATATCTTGGCTCA 1224
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 QY 1225 GATGAATTTAGCAGAGCGAGGCTCTCCAGCAGAGACAT- TTTGCTGGAAGAGTACTGA 1283
 DB 601 GATGAATTTAGCAGAGCGAGGCTCTCCAGCAGAGACATATATTTTGTGAGAGGCTACCGA 660
 QY 1284 TAAAGTGAAGAACTTTATGAGAAACAAATTCAGAGGCGAGAAATCTTTGATGAGTC 1343
 DB 661 TAAATGAGAAATCTTTATGAGAAACAA- -TACTAGGCGAGAAAGCTTTGATGAGCA 717
 QY 1344 AGAGAAAGGTGTACCA 1359
 DB 718 GAGAAAGCGTGACAG 733

RESULT 7
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 LOCUS EST583527 tomato breaker fruit Lycopersicon esculentum cDNA clone
 DEFINITION CB84731 5' end, mRNA sequence.
 ACCESSION BM409200
 VERSION BM409200.1 GI:18260830
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 682)
 AUTHORS Alcala,J., Vrebalov,J., White,R., Vision,T., Karanymcheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Uteback,T., Van Aken,S., Romling,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
 TITLE Generation of ESTs from tomato fruit tissue, breaker stage (2002)
 JOURNAL Unpublished
 COMMENT Contact: CUGI
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: http://www.genome.clemson.edu/orders/index.html
 This clone is available through the Clemson University Genomics Institute
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 /clone_lib="tomato breaker fruit"
 /note="Vector: pBluescriptSKmcdapt; Site 1: EcoRI, Site 2: XhoI; supplier: Boyce Thompson Institute; fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
 BASE COUNT 217 a 114 c 173 g 178 t
 ORIGIN
 Query Match 31.3%; Score 541.2; DB 12; Length 682;
 Best Local Similarity 87.1%; Pred. No. 4.6e-124;
 Matches 594; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
 QY 706 GCAGGTATGCAAGACATTTTCTTAGACCAAGCTATATACCCGAGAGAAAGCA 765
 DB 1 GCAGGTATGCAAGACATTTTCTTAGACCAAGCTATATACCCGAGAGAAAGG 60

QY 766 GCTATCTGGCAATATATATGTGTGTCAGAGAAAGCAAGATGCTTGTATGTCCTPAT 825
 DB 61 GCTATCTGGCAATATATATGTGTGTCAGAGAAAGCAAGATGCTTGTATGTCCTCAA 120
 QY 826 GCATCCACATTAATCTCCGCAAGCTTTAGATAGTGGAGACACAGGCTGGAAATATTTTC 885
 DB 121 GCATCATATATATTAATCCCGGCGAGCTTGAATAGGGGAGAAATAGGCTGAGAAAGTTTC 180
 QY 886 AGTGGGCGGCACTTGTATATGCTTGTATGCTTATCCGATCTCTCAGATTTTCT 945
 DB 181 AATGGGCGGCACTTGTATATGCTTGTATGCTTATCCGATCTCTCAGATTTTCCA 240
 QY 946 GTTGATATTCAGCCATTGAGATATATGAGAAATGCGATGACTGTGGAATTC 1005
 DB 241 GTTGATATTCAGCCATTGAGATATATGAGAAATGCGATGACTGTGGAATTC 300
 QY 1006 AGATACAAACTTTCGATGAGCTATATCTGATTTATGTTGCTGTGACTGTGGA 1065
 DB 301 AGATACAAACTTTCGATGAGCTATATCTGATTTATGTTGCTGTGACTGTGGA 360
 QY 1066 TTGATGAGTGTTCAGTTATGAGTATGCACTGATCAAGCAAGCAAGCAAGAGTGA 1125
 DB 361 TTGATGAGTGTTCAGTTATGAGTATGCACTGATCAAGCAAGCAAGCAAGAGTGA 420
 QY 1126 TATATGCTGCTTGGCTTTAGGCTTGCAATCACTAATCAATATATCTCAGATGTA 1185
 DB 421 TATATGCTGCTTGGCTTTAGGCTTGCAATCACTAATCAATATATCTCAGATGTT 480
 QY 1186 GGAAGAGTCCAGAGAGAGAGAGATATCTTGGCTCAAGATGAATTTAGCAGAGCGG 1245
 DB 481 GGAAGAGTCCAGAGAGAGAGAGATATCTTGGCTCAAGATGAATTTAGCAGAGCGG 540
 QY 1246 CTCTCCGAGCAAGCATATTTGCTGAGAGAGTACTGATAGTGGAGAACTTTATGAAG 1305
 DB 541 CTATCCCATGAGATATATTTGCTGAGAGGCTGACGATATATGAGAAATTTTATGAAG 600
 QY 1306 AAACAAATTCAGAGGCGAGAGAAATTTTGTATGATGTCAGAGAAAGTGTACAGAACTG 1365
 DB 601 AAACAAATTCAGAGGCGAGAGAAATTTTGTATGATGTCAGAGAAAGTGTACAGAACTG 660
 QY 1366 GACTCTGCTATGATGAGCTCTG 1387
 DB 661 AGCTCAGCTATGATGATTCCTG 682

RESULT 8
 AM442407 672 bp mRNA linear EST 18-MAY-2001
 LOCUS EST311803 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
 DEFINITION clone CLEN22L14 5', mRNA sequence.
 ACCESSION AM442407
 VERSION AM442407.1 GI:6977658
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 672)
 AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ann,S., Romling,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
 TITLE Generation of ESTs from tomato fruit tissue
 JOURNAL Unpublished
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: http://www.genome.clemson.edu/orders/index.html
 5 prime sequence.
 FEATURES
 source location/Qualifiers
 1..672
 /organism="Lycopersicon esculentum"


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/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEB2L14"
/tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/clone_lib="tomato fruit red ripe, TAMU"
/notes="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Giovannoni; Fruit were tagged at the
breaker stage (first sign of lycopen accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."

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BASE COUNT 212 a 112 c 170 g 178 t

ORIGIN

Query Match 30.8%; Score 532.8; DB 9; Length 672;
 Best Local Similarity 87.1%; Pred. No. 5.8e-122;
 Matches 585; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

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719 AGACATTTTACTTGAAGAACCAAGCTAATGACCCAGAGAGAAAGAGCTATCTGGGCAA 778
1 AGACCTTTAACTTGAAGAACTATGATGACCTCCGAGAGAAAGAGGCTATCTGGGCAA 60
779 TATATGTGTGTCGAGAGAGAGAGAGAGCTTGTGATGAGCCCTAATGATCCCAATTA 838
61 TATATGTATGTGTCGAGAGAGAGAGAGAGAGCTTGTGATGAGCCCAATGATATTA 120
839 CTCCGCAAGCTTTAGATAGTGGGAGACGAGCTGGAGATATTTTCAAGTGGGCGCCAT 898
121 CCCCGGAGCCCTTATAGTAGTGGGAAATAGGCTAGAAATGTTTCAATGGGCGCCAT 180
899 TTGATATGCTTATGCTGCTTTATCCGATACGTCTCCAGATTTTCCGTGATATTCACG 958
181 TTGACATGCTCATGATGCTTGTGTCGATACAGTTTCACTTCAGTTGATATTCACG 240
959 CATTGAGAGATGATGATGAGAGAGAGAGAGAGAGCTTGTGATGAGAGAGAGAGAGAG 1018
241 CATTGAGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
1019 TCGATAGCTATATCTTATGTTTACTATGTTGCTGTGATGCTGATGATGATGCTTC 1078
301 TCGAGAGACTATATCTTATGTTTACTATGTTGCTGTGATGCTGATGATGATGCTTC 360
1079 CAGTTATGGGATGTCACCTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1138
361 CATTATGGGATGTCGCTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
1139 TGGCTTATGGGCTTGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1198
421 TGGCTTATGGGCTTGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 480
1199 GAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1258
481 GAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
1259 ACATATTTGCTGGAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1318
541 ATATATTTGCTGGAAGAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 600
1319 GGGGCAAGAGATTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1378
601 GGGGCAAGAGATTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
1379 GATGGCTGTGT 1390
661 GATTCCTGTAT 672

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RESULT 9

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BE433198
LOCUS BE433198 642 bp mRNA linear EST 18-MAY-2001
DEFINITION EST399727 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
ACCESSION BE433198
VERSION BE433198.1 GI:9431041
SOURCE BE433198.1
ORGANISM Lycopersicon esculentum (tomato)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 642)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Niernman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
,S.D.
Generation of ESTs from tomato fruit tissue, breaker stage
JOURNAL Unpublished
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
source
1..642
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEB12N5"
/tissue_type="pericarp"
/dev_stage="breaker"
/lab_host="SOL"
/clone_lib="tomato breaker fruit, TIGR"
/notes="Vector: pBlueScriptSMCtdapt; Site 1: EcoRI;
Site 2: XhoI; Fruit were harvested at the breaker stage
(first sign of lycopen accumulation on the blossom end of
the fruit). Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
BASE COUNT 194 a 103 c 167 g 178 t
ORIGIN
Query Match 30.2%; Score 522; DB 10; Length 642;
Best Local Similarity 88.3%; Pred. No. 2.8e-119;
Matches 567; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
660 TTTGGGCTTTGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 719
1 TTTGGGCTTTGAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
720 GACATTTTACTTGAAGAACCAAGCTAATGACCCAGAGAGAGAGAGAGAGAGAGAGAG 779
61 GACGTTTAACTTGAAGAACTATGATGATGATGATGATGATGATGATGATGATGATGAT 120
780 ATATGCTGTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839
121 ATATGCTGTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
840 TCCGCAAGCTTTAATAGAGTGGAGAGACCGAGAGAGATATTTTCAAGTGGGCGCCAT 899
181 CCCGCAAGCTTTAATAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
900 TGATATGCTTATGCTGCTTTATCCGATACGTCTCCAGATTTCTGTTGATATTCAGCC 959
241 TGACATGCTCATGATGCTTGTGTCGATACAGTTTCACTTCAGATTTGATATTCAGCC 300
960 ATTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1019
301 ATTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
1020 CGATGAGCTATATCTTATGTTTACTATGTTGCTGTGATGATGATGATGATGATGCTTC 1079

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Db 361 CGAGCAATATACCTTTATGTTATTTATGTTGCTGTGATCGTTGGCTGATGAGTGTCC 420
 Oy 1080 AGTATGGGTATGTGACCTGAATCAAGGCAACACAGAGCTATATATGCTGCTT 1139
 Db 421 AATTATGGGTATCGCCCTGAATCAAGGCAACACAGAGCTATATATGCTGCTT 480
 Oy 1140 GCGTTTATGGGCTTGCAATCACTAACCAATATCTCAGAGATGAGAGAGATGCCAG 1139
 Db 481 GCGCTGTGGGATCGCAATCACTTAATCACTTCTCAGAGATGTTGAGAGAGATGCCAG 540
 Oy 1200 AAGGAGAGATATCTTGTCTCAAGATGATGACACAGAGGCTCTCCAGCAAGA 1239
 Db 541 AAGGAGAGATCTACTGCTCCCAAGATGATGACACAGAGGCTCTATCCGATGAAGA 600
 Oy 1260 CATATTTGCTGGAAGATGATGATGATGAGAGAGCTTAT 1301
 Db 601 TATATTTGCTGGAAGGATGACGATTAATGAGAAATCTTAT 642

RESULT 10

LOCUS AM222027 676 bp mRNA linear EST 18-MAY-2001
 DEFINITION EST298838 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
 clone cLEN6L15, mRNA sequence.

ACCESSION

AM222027

VERSION

AM222027.1

KEYWORDS

GI:6533711

SOURCE

EST.

ORGANISM

Lycopersicon esculentum (tomato)

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 676)

AUTHORS

Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
 Upson,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Renning,C.M.,
 Frazer,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
 Generation of ESTs from tomato fruit tissue
 Unpublished

TITLE

Contact: CUGI

JOURNAL

Clemson University Genomics Institute

COMMENT

100 Jordan Hall, Clemson, SC 29634, USA
 Email: http://www.genome.clemson.edu/orders/index.html
 5 prime sequence.

FEATURES

Location/Qualifiers

1..676

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="cLEN6L15"

/issue_type="pericarp"

/dev_stage="red ripe (7-20 days post-breaker)"

/clone_1b="tomato fruit red ripe, TAMU"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
 XhoI; supplier: Giovannoni; Fruit were tagged at the
 breaker stage (first sign of lycopen accumulation on the
 blossom end of the fruit) and harvested 7 days
 post-breaker (fully red-ripe), 10 days post breaker, and
 20 days post-breaker (over-ripe). 20 day fruit which
 showed external or internal signs of pathogenesis were
 discarded. Fruit were cut in half and the seeds and
 locules were discarded prior to freezing the pericarp."

BASE COUNT

214 a 118 c 165 g 179 t

ORIGIN

Query Match 29.8%; Score 515.8; DB 9; Length 676;
 Best Local Similarity 85.5%; Pred. No. 1e-117;
 Matches 574; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

Oy

808 CTTGTATGGCCCTAATGATCCACATTAACCTCGCAAGCTTATGATAGGTGGAGACC 867
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Db 2 CTTGTATGAGCCCAAAAGCATATATATATCCCGGACCTTAGATAGTGGAGAAAT 61
 Oy 868 AGGCTGAGAGATATTTTCACTGAGGCGGCCATTTGATATGCTGATGCTTATCCGAT 927
 Db 62 AGGCTGAGAGATTTTTCATATGCGCGCCATTTGACATGCTCATGCTGCTTGTCCGAT 121
 Oy 928 ACTGTCTCAGATTTTCTGTGTATATTCAGCCATTCAGATATGATGAGAGAAATCGT 987
 Db 122 ACAGTTTCTAATCTTCCAGTTGATATTCAGCCATTCAGATATGATGAGAGAAATCGT 181
 Oy 988 ATGACCTTGTGAAATTCAGATCAAAACTTTGATGAGAGTATATCTTATCTAT 1047
 Db 182 ATGACCTTGTGAAATTCAGATCAAAACTTTGATGAGAGTATATCTTATCTAT 241
 Oy 1048 GTTGTCTGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1107
 Db 242 GTTGTCTGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 301
 Oy 1108 GCAACAAACAGAGAGTATATATATGCTGCTTTGAGGCTTGCAATCAATCAACC 1167
 Db 302 GCAACAAACAGAGAGTATATATATGCTGCTTTGAGGCTTGCAATCAATCAATCAACT 361
 Oy 1168 AATATATCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1227
 Db 362 AATATATCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 421
 Oy 1228 GAATTTACACAGAGAGGCTCTCCGACGAGACATATTTGCTGAGAGAGTATGATGATGAT 1287
 Db 422 GAATTTACACAGAGAGGCTCTATCCGATGATGATGATGATGATGATGATGATGATGAT 481
 Oy 1288 TGGAGAACTTTTATGAGAAACAAATTCAGAGGCGGAGAAATTTTATGATGATGATGAT 1347
 Db 482 TGGAGAACTTTTATGAGAAACAAATTCATAGGCAAGAAAGTTCTTATGATGATGATGAT 541
 Oy 1348 AAGAGTCTCAGACATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1407
 Db 542 AAGAGTCTCAGACATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 601
 Oy 1408 TATGCAAGATTTTATGAGAGATTTGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1467
 Db 602 TATGCAAGATTTTATGAGAGATTTGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 661
 Oy 1468 TATGTTAGCAA 1478
 Db 662 TATGTTAGCAA 672

RESULT 11

LOCUS BM412533 634 bp mRNA linear EST 22-JAN-2002
 DEFINITION EST586860 tomato breaker fruit Lycopersicon esculentum cDNA clone
 cLEG60114 5' end, mRNA sequence.

ACCESSION

BM412533

VERSION

BM412533.1

KEYWORDS

GI:18264163

SOURCE

EST.

ORGANISM

Lycopersicon esculentum (tomato)

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 634)

AUTHORS

Alcala,J., Vrebalov,J., White,R., Viston,T., Karameycheva,S.A., Tsai
 J., Bouari,O., Kirkness,E., Uteback,T., Van Aken,S., Renning
 C.M., Frazer,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
 Generation of ESTs from tomato fruit tissue, breaker stage (2002)

TITLE

Unpublished

JOURNAL

Contact: CUGI

COMMENT

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA
 Email: http://www.genome.clemson.edu/orders/index.html
 This clone is available through the Clemson University Genomics
 Institute

FEATURES

source

Seq primer: T3.

Location/Qualifiers

1..634

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="CIEG60114"

/tissue_type="Pericarp"

/dev_stage="breaker"

/lab_host="SOLR"

/note="Vector: pBluescriptSkmUdapt; Site 1: EcoRI;

Site 2: XhoI; supplier: Boyce Thompson Institute;

sequencing: The Institute for Genomic Research; Fruit

were harvested at the breaker stage (first sign of

lycopene accumulation on the blossom end of fruit). Fruit

were cut in half and the seeds and locules were discarded

prior to freezing the pericarp."

BASE COUNT 200 a 105 c 160 g 169 t

ORIGIN

Query Match 28.8%; Score 498.2; DB 12; Length 634;
 Best Local Similarity 87.6%; Pred. No. 2.5e-113;
 Matches 556; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

706 GGAGATGCAAGACATTTTACTAGAACCAAGCTAATGACCCGAGAGAAAGAA 765

1 GGAGATGCAAGACATTTTACTAGAACCAAGCTAATGACCCGAGAGAAAGAA 60

766 GGTATCGGCAATATATGCTGTGTCAGAGAACGATGAGCTTGTGATGCCCTAAT 825

61 GGTATCGGCAATATATGCTGTGTCAGAGAACGATGAGCTTGTGATGCCCTAAT 120

826 GCATCCCAATATCTCCGAGCTTATGATGCTGGAACCAAGCTTGAATATTTTC 885

121 GCATCATATATATACCCCGAGCTTATGATGCTGGAACCAAGCTTGAATATTTTC 180

886 AGTGGCGGCAATTTGATGCTGTGTCAGAGAACGATGAGCTTGTGATGCCCTAAT 945

181 AATGGCGGCAATTTGATGCTGTGTCAGAGAACGATGAGCTTGTGATGCCCTAAT 240

946 GTTGATATTCAGCATTCAGAGATGATGATGATGATGATGATGATGATGATGATG 1005

241 GTTGATATTCAGCATTCAGAGATGATGATGATGATGATGATGATGATGATGATG 300

1006 AATACCAAACTTTCAGATGATGATGATGATGATGATGATGATGATGATGATG 1065

301 AATACCAAACTTTCAGATGATGATGATGATGATGATGATGATGATGATGATG 360

1066 TTGATGATGCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATG 1125

361 TTGATGATGCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATG 420

1126 TATTAATGCTGCTTTGCTTTAGGCTTGAAGAAATCACTAACCAATATATCTCAGAGATG 1185

421 TATTAATGCTGCTTTGCTTTAGGCTTGAAGAAATCACTAACCAATATATCTCAGAGATG 480

1186 GGAGAGATGCAAGAGAGAGAGATATCTTGCCTCAAGATGAATTAACACAGGAGG 1245

481 GGAGAGATGCAAGAGAGAGAGATATCTTGCCTCAAGATGAATTAACACAGGAGG 540

1246 CTCTCCGAGAGACATATTTGCTGGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1305

541 CTATCCGAGAGAGATATATTTGCTGGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 600

1306 AAAACAATTCAGAGGCGAGAAATCTTTGATGA 1340

601 AAAC-AATACATAGGGGAGAAAGTTCTTGAATGA 634

RESULT 12
 BI921390

LOCUS BI921390 599 bp mRNA linear EST 17-OCT-2001

DEFINITION EST541293 tomato callus Lycopersicon esculentum cDNA clone CIEC73K6

5' end. mRNA sequence.

ACCESSION BI921390

VERSION BI921390.1 GI:16217418

KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asterids; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

Alcala,J., Vrebalov,J., White,R., Vision,T., Karanymcheva,S.A., Tsai

J., Uteback,T., Van Aken,S., Romling,C.M., Fraser,C.M., Martin

G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato callus tissue (2001)

Generation of ESTs from tomato callus tissue (2001)

Unpublished

CONTACT: CUGI

COMMENT: Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics

Institute

Seq primer: T3.

Location/Qualifiers

1..599

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TA496"

/db_xref="taxon:4081"

/clone="CIEC73K6"

/tissue_type="callus"

/dev_stage="25-40 days old"

/lab_host="XLI-Blue MRP"

/clone_lib="tomato callus"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:

XhoI; supplier: Boyce Thompson Institute; sequencing: The

Institute for Genomic Research; cIEC - Cotyledons of

seedlings 7-10 days post-germination were excised, cut at

both ends and placed on MS medium with no selection. Mixed

callus was harvested at 25 and 40 days and included

undifferentiated masses. Tomato Callus EST Library"

BASE COUNT 170 a 89 c 178 g 162 t

ORIGIN

Query Match 28.2%; Score 487.2; DB 12; Length 599;
 Best Local Similarity 89.3%; Pred. No. 1.4e-110;
 Matches 536; Conservative 0; Mismatches 63; Indels 1; Gaps 1;

275 TTTCTCCCACTTCCGAGCTTTCGAAATGGAACAGATTGTTGATTCAGTCCGAGAGAA 334

1 TTTCTCCCACTTCCGAGCTTTCGAAATGGAACAGATTGTTGATTCAGTCCGAGAGAA 60

335 ACCGGCTCTTTGATCATCCAGGCTTCAGTCCGAGATGAGAAATTTGATGAGATGGA 394

61 ACCGGCTCTTTGATCATCCAGGCTTCAGTCCGAGATGAGAAATTTGATGAGATGGA 120

395 GAATCAAGAAAGTGGAGAGACAAAGGTGAATTTGGCTCTTTAATTCGATCCAGAT 454

121 GAATCAAGAAAGTGGAGAGACAAAGGTGAATTTGGCTCTTTAATTCGATCCAGAT 180

455 ATTCAATGCTTGGGTGATCAAGAAATGAAAGGAGACATTTCTCTGATCAGTCCAGTT 514

181 ATTCAATGCTTGGGTGATCAAGAAATGAAAGGAGACATTTCTCTGATCAGTCCAGTT 240

515 TGGGGCTAGCCAGCTGGAAGAAATGATGATGATGATGATGATGATGATGATGATG 574

241 TGGGGCTAGCCAGCTGGAAGAAATGATGATGATGATGATGATGATGATGATGATG 299

575 TATTAAGCAGGACGCTTATGTAAGAGAGAGCTGATCTTACCGATGATTTAGAAATGA 634

300 TATTAAGCAGGACGCTTATGTAAGAGAGAGCTGATCTTACCGATGATTTAGAAATGA 359

QY 635 AGCCGATATTTGTTGTCAGGGAATTTGGCTTGTGAGTGAACATATGATCGTTTG 694
 DB 360 AGCCGATATTTGTTGTCAGGGAATTTGGCTTGTGAGTGAACATATGATCGTTTG 419
 QY 695 GCGAATATGTCAGAGTATGCAAGACATTTTACTTAGAGAACCAAGCTTAATGACCCAG 754
 DB 420 GCGAATATGTCAGAGTATGCAAGACATTTTACTTAGAGAACCAAGCTTAATGACCCAG 479
 QY 755 AGAGAAGAAAGCTATCTGGGCAATATATGTTGTGAGAGAGAACGATGAGCTTGTG 814
 DB 480 ACAGAAGAAAGCTATCTGGGCAATATATGTTGTGAGAGAGAACGATGAGCTTGTG 539
 QY 815 ATGGCCCTAATGATCCACATTAACCTCCGCAAGCTTTAGATAGTGGAGACAGAGCTG 874
 DB 540 ATGGCCCTAATGATCCACATTAACCTCCGCAAGCTTTAATAGTGGAGAGAGCTG 599

 RESULT 13
 BE460889 600 bp mRNA linear EST 18-MAY-2001
 LOCUS EST412308 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
 DEFINITION clone CLEB36H12, mRNA sequence.
 ACCESSION BE460889
 VERSION BE460889.1 GI:9505191
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 600)
 AUTHORS Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Roming,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
 TITLE Generation of ESTs from tomato fruit tissue, breaker stage
 JOURNAL Unpublished
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.
 FEATURES
 SOURCE 1.600
 location/Qualifiers
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="TA496"
 /db_xref="taxon:4081"
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 /tissue_type="Pericarp"
 /dev_stage="breaker"
 /lab_host="SOLR"
 /clone_lib="tomato breaker fruit, TIGR"
 /note="Vector: pBluescriptKmc2adap; Site 1: EcoRI; Site 2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
 BASE COUNT 178 a 99 c 157 g 166 t
 ORIGIN
 Query Match 28.1%; Score 486.4; DB 10; Length 600;
 Best Local Similarity 88.2%; Pred.No. 2.2e-110;
 Matches 529; Conservative 0; Mismatches 71; Indels 0; Gaps 0;
 QY 650 TTCGAGGGAATTTGGCTTGTGAGTGAAGCATATGCTTGGCGAAGATGTGAG 709
 DB 1 TTCGAGGGAATTTGGCTTGTGAGTGAAGCATATGCTTGGCGAAGATGTGAG 60
 QY 710 AGTATGCAAGACATTTTACTTAGAGAACCAAGCTAATGACCCAGAGAGAGAGCTA 769

DB 61 AGTATGCAAGACATTTTACTTAGAGAACCAAGCTAATGACCCAGAGAGAGAGCTA 120
 QY 770 TTCGAGGGAATTTGGCTTGTGAGTGAAGCATATGCTTGGCGAAGATGTGAG 829
 DB 121 TTCGAGGGAATTTGGCTTGTGAGTGAAGCATATGCTTGGCGAAGATGTGAG 180
 QY 830 CCACATTAATCTCCGCAAGCTTTAGATAGTGGAGACAGAGCTGGAAGATATTTCAATG 889
 DB 181 CATATTAATCTCCGCAAGCTTTAGATAGTGGAGAAATAGGCTAAGAGATGTTTCAATG 240
 QY 890 GCGGCAATTTGATATATCTGATGCTTATCCGATCTGCTGCTGCTGCTGCTGCTG 949
 DB 241 GCGGCAATTTGATATATCTGATGCTTATCCGATCTGCTGCTGCTGCTGCTGCTG 300
 QY 950 ATATTGACCATTCAGAGATATGATTAAGAGAAATGCTATGACTTGTGAAATCCAGAT 1009
 DB 301 ATATTGACCATTCAGAGATATGATTAAGAGAAATGCTATGACTTGTGAAATCCAGAT 360
 QY 1010 ACAAACTTTGATGACCTATATCTTATTTGTTAATGTTGCTGTTACTGTAGATTTGA 1069
 DB 361 ACAAACTTTGATGACCTATATCTTATTTGTTAATGTTGCTGTTACTGTAGATTTGA 420
 QY 1070 TGAATGTCAGATATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1129
 DB 421 TGAATGTCAGATATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 1130 ATGCTGCTTTGGCTTTAGGCTTGGCTTGGCAATCACTAATCACTAATCACTAATCACT 1189
 DB 481 ATGCTGCTTTGGCTTTAGGCTTGGCTTGGCAATCACTAATCACTAATCACTAATCACT 540
 QY 1190 AAGATGCGAAGAGAGAGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1249
 DB 541 AAGATGCGAAGAGAGAGATATGATGATGATGATGATGATGATGATGATGATGATGAT 600

 RESULT 14
 BE432511 623 bp mRNA linear EST 18-MAY-2001
 LOCUS EST399040 tomato breaker fruit, TIGR Lycopersicon esculentum cDNA
 DEFINITION clone CLEB8H5, mRNA sequence.
 ACCESSION BE432511
 VERSION BE432511.1 GI:9430354
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 623)
 AUTHORS Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Roming,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
 TITLE Generation of ESTs from tomato fruit tissue, breaker stage
 JOURNAL Unpublished
 COMMENT Contact: CUGI
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Email: <http://www.genome.clemson.edu/orders/index.html>
 5 prime sequence.
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 /clone="CLEB8H5"
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 /lab_host="SOLR"
 /clone_lib="tomato breaker fruit, TIGR"
 /note="Vector: pBluescriptKmc2adap; Site 1: EcoRI;

Site 2: XhoI; Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

BASE COUNT

191 a 101 c 164 g 167 t

ORIGIN

Query Match 28.0%; Score 483.4; DB 10; Length 623;
Best Local Similarity 87.2%; Pred. No. 1.2e-109;
Matches 543; Conservative 0; Mismatches 76; Indels 4; Gaps 1;

QY 674 GTGAAGCATATGATCTGTTGGCGAAGTATGTGCAGATGTGCAAGACATTTTACTTAG 733
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QY 734 GAACCAAGTATGACCCGAGAGAGAAAGCATCTGGGCAATATATGTGTGTGA 793
DB 61 GAACTATGTATGATGATCCCGAGAGAGAGGCTATCTGGGCAATATATGATGTGTGA 120
QY 794 GGAGAACGATGATGTTGTGATGGCCCTATATGATCCCATTAATCTCCGCAAGCTTTAG 853
DB 121 GAAAGAACATGATGATGTTGTGATGGCCCAAGGATCATATATATCCCGGAGAGCTTTAG 180
QY 854 ATAGGTGGAGACAGGCTGGAAGATATTTTCAATGTGGCCGCAATTTGATATGCTTGATG 913
DB 181 ATAGGTGGAGAAATAGGCTGGAAGATGTTTCAATGTGGCCGCAATTTGATATGCTTGATG 240
QY 914 CTGCTTATCCGATCTGCTCCAGATTTCTGTTGATTTTCAAGCATTCAGAGATATTA 973
DB 241 GTGCTTTGTCGATATGATTTTCACTTTCAGTTGATATTAATTCAGCATTCAGAGATATTA 300
QY 974 TTGAAGGATGCGTATGATGATGTTGGAATCCAGATACAAATCTTCATGAGCTATATC 1033
DB 301 TTGAAGGATGCGTATGATGATGTTGGAATCCAGATACAAATCTTCATGAGCTATATC 360
QY 1034 TCTATTTGTTAC---TATGTTGCTGTGCTGATGATGATGATGATGATGATGATGATG 1089
DB 361 TTTATTTGTTAATTTATTTATGTTGCTGTTGCTGTTGCTGTTGCTGTTGCTGTTGCT 420
QY 1090 ATTGACCTGATTCGAAAGGCAACAGAGATGTTATATGCTGCTTGGCTTTAGGG 1149
DB 421 ATGCCCCCTGAAATCAAGGCAACAGAGATGTTATATGCTGCTTGGCTTTAGGG 480
QY 1150 CTTCGAATCACTAATCAATATCTAGAGATGTGAGAGAGATGCCAGAGAGAGAGA 1209
DB 481 ATGCAATCACTAATCAATATCTAGAGATGTGAGAGAGATGCCAGAGAGAGAGA 540
QY 1210 GTATACCTGCTCAAGATGATTAAGACAGAGGCTCTCCAGACAGACATATTTGCT 1269
DB 541 GTCTACTGCTCAAGATGATTAAGACAGAGGCTCTATCCGATGAAATATTTGCT 600
QY 1270 GGAAGATGATGATTAAGAG 1292
DB 601 GGAAGGTTGACCGATTAATGAG 623

RESULT 15

AW221932

LOCUS AW221932 685 bp mRNA linear EST 18-MAY-2001

DEFINITION EST98743 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA

ACCESSION

AW221932

VERSION AW221932.1 GI:6533616

KEYWORDS

SOURCE

ORGANISM

EST

LYCOPERSICON ESCULENTUM (tomato)

LYCOPERSICON ESCULENTUM

EUKARYOTA; VIRIDIPHYTES; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 685)

Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,

Upton,D., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Romming,C.M.,

Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.

TITLE
JOURNAL
COMMENT

Generation of ESTs from tomato fruit tissue
Unpublished
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
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/clone_1b="tomato fruit red ripe, TAMU"

/note="Vector: pBluescript SK(-); Site 1: EcoRI, Site 2: XhoI; supplier: Giovannoni; Fruit were tagged at the breaker stage (first sign of lycopene accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

BASE COUNT

237 a 113 c 150 g 185 t

ORIGIN

Query Match 27.7%; Score 478.8; DB 9; Length 685;
Best Local Similarity 84.7%; Pred. No. 1.8e-108;

Matches 537; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 928 ACTGTCTCAAGATTTCTGTTGATATTCAGCCATTCAGAGATGATGAAGAAATGCGT 987
DB 1 ACAGTTTCTAATCTTCCAGTTGATATTCAGCCATTCAGAGATGATGAAGAAATGCGT 60
QY 988 ATGACCTTGGAATTCAGATACAAATCTTCATGAGCTATATCTATTTGTTACTAT 1047
DB 61 ATGACCTTGGAATTCAGATACAAATCTTCATGAGCTATATCTATTTGTTACTAT 120
QY 1048 GTTGTGCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1107
DB 121 GTTGTGCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 1108 GCACACAGAGATGATATATGCTGCTTTAGGGCTTGCAATCACTAAC 1167
DB 181 GCACACAGAGATGATATATGCTGCTTTAGGGCTTGCAATCACTAAC 240
QY 1168 AATATATCTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1227
DB 241 AACATATCTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
QY 1228 GAATTAGACAGAGGAGGCTCTCCGACAGACATATTTGCTGGAAGATGCTGATAG 1287
DB 301 GAATTAGACAGAGGAGGCTCTATCCGATGAAATATTTGCTGGAAGATGCTGATAG 360
QY 1288 TGAAGAACTTTATGAAGAAACAAATTCAGAGGGGAGAAATCTTTGATGATGATG 1347
DB 361 TGAAGAACTTTATGAAGAAACAAATTCAGAGGGGAGAAATCTTTGATGATGATG 420
QY 1348 AAAGGTGTCAGAACTGATCTGCTAGTATGATGATGATGATGATGATGATGATG 1407
DB 421 AAAGGTGTCAGAACTGATCTGCTAGTATGATGATGATGATGATGATGATGATG 480
QY 1408 TATCGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1467
DB 481 TATCGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
QY 1468 TATGTTAGCAAGCAAGAACTTCTCACTTGGCCATTTGTTATGCAAAATCTCTTGTG 1527
DB 541 TATGTTAGCAAGCAAGAACTTCTCACTTGGCCATTTGTTATGCAAAATCTCTTGTG 600

Oy 1528 CCCCCTAATAGAACTTCTCTCTCACTAGCAAGA 1561
||| |
Db 601 CTTCTACAAAAAATGCTCTCTCTTCAAGATATA 634

Search completed: January 16, 2004, 04:04:17
Job time : 3751 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 16, 2004, 04:06:36 ; Search time 5040 Seconds
(without alignments)
3571.475 Million cell updates/sec

Title: US-09-847-081b-2

Perfect score: 2270

Sequence: 1 MSMSVALLMVVSPITSEVNSG.....IAYAKSLVPPNRTSSPLAKT 440

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=genembi -QFMT=fastap -SUFFIX=rge -MTNMatch=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIG=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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15:	em_ba:*
16:	em_fun:*
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27:	em_scs:*
28:	em_un:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2192.5	96.6	1573	6	AX657549
2	1827	80.5	1295	8	CAPSYL
3	1751	77.1	1786	8	TOMCBPE
4	1750	77.1	1239	6	A68204
5	1750	77.1	1239	6	AR156064
6	1750	77.1	1239	6	BD005486
7	1744	76.8	1239	6	A68203
8	1744	76.8	1239	6	AR156063
9	1744	76.8	1239	6	BD005485
10	1733	76.3	1614	8	LERIPE
11	1732	76.3	1646	6	A21360
12	1732	76.3	1646	6	AR007503
13	1668	71.5	1355	8	LERYGTOMS
14	1626	71.6	1506	8	AF220218
15	1626	71.6	1689	8	AB037975
16	1606	70.7	1773	8	AF152892
17	1598	70.4	1637	8	HAN308385
18	1595	70.3	2868	6	E15683
19	1590	70.0	1598	8	HAN304825
20	1580.5	69.6	1376	8	AY099482
21	1568.5	69.1	1576	8	CMPSTYMR
22	1568	69.1	1371	8	AP251015
23	1559.5	68.7	1372	6	A48337
24	1557	68.6	1921	6	E15681
25	1544.5	68.0	1853	8	AY056287
26	1542	67.9	1269	6	AX506034
27	1542	67.9	1472	8	BT002084
28	1542	67.9	1703	8	AY085565
29	1542	67.9	1757	8	BT000450
30	1531	67.4	2085	6	E15680
31	1530	67.4	1119	8	TOMPSY2A
32	1526.5	67.2	1769	6	ATPHYSYN
33	1523	67.1	1932	6	E15682
34	1519	66.9	1548	8	NPPSY
35	1495.5	65.9	4073	8	LESPFS
36	1431.5	63.1	1304	6	AX350858
37	1334.5	58.8	1538	8	AB032797
38	1282.5	56.5	3707	8	LEGTOMS
39	1268.5	55.9	3200	8	AP009954
40	1268.5	55.9	3200	8	AB005238
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42	1064	46.9	681	8	AF196963
43	1059	46.7	686	8	AF158024
44	1054.5	46.5	1278	8	DB091900
45	1052	46.3	1859	8	AP305430

RESULT 1

ALIGNMENTS

AX657549 1573 bp DNA linear PAT 24-MAR-2003

LOCUS AX657549 Sequence 3 from Patent WO02103021.

DEFINITION AX657549

ACCESSION AX657549.1 GI:29169361

VERSION

KEYWORDS

SOURCE Nicotiana tabacum (common tobacco)

ORGANISM Nicotiana tabacum

REFERENCE 1 Sandmann, G., Ruemer, S., Luebeck, J., Adomat, C. and Kauder, F. Method for increasing the carotenoid-content in transgenic plants Patent: WO 02103021-A 3 27-DEC-2002;

JOURNAL Von kameke, Kartz (DE)

FEATURES

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BASE COUNT 472 a 270 c 390 g 435 t 6 others

ORIGIN

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Pred. No.: 1.57e-179 Length: 1573

Score: 2192.50 Matches: 427

Percent Similarity: 97.51% Conservative: 3

Best Local Similarity: 96.83% Mismatches: 10

Query Match: 96.59% Indels: 1

DB: 6 Gaps: 1

US-09-847-081b-2 (1-440) x AX657549 (1-1573)

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DB 70 ACAGATTCTTGATTCAGTCCGAGATGAGAAACCGCTTTGTATCATCCAGTTCTCTA 129

QY 41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgGlyLeuGlyGly---ArgGlnArg 59

DB 130 GCTCGAGGTAGCAATTTGATGATGAGATGAGCAATCAAGAAAGCGGAGACGACAAAG 189

QY 60 TrpAsnPheGlySerLeuLeuLeuAlaAspProArgTrpSerCysLeuGlyGlySerArgThr 79

DB 190 TGGAAATTTGGCTTTTAATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 249

QY 80 GluLysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMet 99

DB 250 GANNNTGGAAGACATTTCTCTGTACAGTCCAGTTGGTGGCTAGCCGAGCTGGAAGAAATG 309

QY 100 ThrValSerSerGluLysValValTrpAspValValLeuLysGlnAlaAlaLeuValLys 119

DB 310 ACTGTGTATCATCAGAAAGAGGTGTATGATGATGATGATGATGATGATGATGATGATG 369

QY 120 ArgGlnLeuArgSerThrAspAspLeuGluValLysProAspIleValValProGlyLys 139

DB 370 AGGCGAGCTGAGATCTACCGATATTAGAGGAAAGCCGAGATATTGTTGTTCCAGGAGAT 429

QY 140 LeuGlyLeuLeuSerGluAlaTrpAspArgCysGlyGluValCysAlaGluTrpAlaLys 159

DB 430 TTGGCTGTTGTTGAGCGAAGCAATATGATCTTTGGCGAAGTATGTCGAGAGTATCAAG 489

QY 160 ThrPheTrpLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIle 179

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DB 610 CCGCAACCTTTAGATAGTGGGAGACACGAGCTGGAATATTTTCACTGGGCGGCAATTT 669

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DB 670 GATATGCTTATGCTGCTTATTCGATATCTGCTCCAGATTTCTGTTGATATTCAGCA 729

QY 240 PheArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTrpLysThrPhe 259

DB 730 TTCAGATATGATGATGAGAAATCGATATGATGATGATGATGATGATGATGATGATGAT 789

QY 260 AspGluLeuTrpLeuTrpCysTrpTrpValAlaGlyThrValGlyLeuMetSerValPro 279

DB 790 GATGAGCTATATCTCTATGTTACTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 849

QY 280 ValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTrpAsnAlaAlaLeu 299

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QY 320 ArgGlyArgValTrpLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAsp 339

DB 970 AGAGGAAGAGTATCTGCTCAAGATGAAATGACAGCAGGCTCTCCGAGAAAGAC 1029

QY 340 IlePheAlaGlyArgValThrAspLysTrpArgAsnMetLysGlnIleGlnArg 359

DB 1030 ATATTTCTGGAAGAGTACGATGATGAGAACTTTATGAAAGAAACAATTCAGAGG 1089

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DB 1150 TGGCTGTGTTAAACAGCGCTGCTGTGTATGCAAGATATGAGCAGATGAAAGCCAAC 1209

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DB 1210 GACTACAAACATTCACAGAGGCTTATGTTAGCAAGCCAAAGAAAGCTTCACTTG 1269

QY 420 ProIleAlaTrpAlaLysSerLeuValProProAsnArgTrpSerSerProLeuAlaLys 439

DB 1270 CCCATGCTTATGCAAAATCTTGTGCCCCCTATAGAACTTCTTCCACTGCAAG 1329

QY 440 Thr 440

DB 1330 ACA 1332

RESULT 2

CAPST1

LOCUS CAPST1 1295 bp mRNA linear PLN 05-FEB-1994

DEFINITION C. annum psy1 mRNA for phytoene synthase.

ACCESSION X68017

VERSION X68017.1 GI:433993

KEYWORDS phytoene synthase.

SOURCE Capsicum annum

ORGANISM Capsicum annum

REFERENCE 1 (bases 1 to 1295) Romer, S., Huguency, P., Bouvier, F., Camara, B. and Kuntz, M. Expression of the genes encoding the early carotenoid biosynthetic enzymes in Capsicum annum

REFERENCE 1 (bases 1 to 1786)
 AUTHORS Bartley,G.B., Vitanen,P.V., Bacot,K.O. and Scolnik,P.A.
 TITLE A tomato gene expressed during fruit ripening encodes an enzyme of
 the carotenoid biosynthesis pathway
 JOURNAL U. Biol. Chem. 267 (8), 5036-5039 (1992)
 MEDLINE 92184738
 PUBMED 1544888
 COMMENT Original source text: Lycopersicon esculentum (library: Clontech
 fruit cDNA) breaker fruit stage fruit cDNA to mRNA.
 location/qualifiers

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CDS
 polyA_site
 BASE COUNT 594 a 259 c 420 g 513 t
 ORIGIN

Alignment Scores:
 Pred. No.: 2.08e-141 Length: 1786
 Score: 1751.00 Matches: 344
 Percent Similarity: 86.67% Conservative: 33
 Best Local Similarity: 79.08% Mismatches: 34
 Query Match: 77.14% Indels: 24
 DB: 8 Gaps: 3

US-09-847-081B-2 (1-440) x TOMCPBE (1-1786)

Qy 1 MetSerMetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGly 20
 Db 308 CTCGAATGTCGTGTCGTGTGTTGGGTGTCTCTCT--TGTGACGTCCTCAATGGG 364

Qy 21 ThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu 40
 Db 365 ACAAGTTTCATGGAATCAGTCGGGAGGGAACCGTTTGTGATTCATCG----- 415

Qy 41 AlaArgAspArgAsnLeuMetTrpAsnGlyValGlyIleValGlyValArgGlnArgTrp 60
 Db 416 ---AGGCATAGGAATTTGCTGTCCCAATGAGAAATCATATAGAGGT----- 457

Qy 61 AsnPheGlySerLeuIleAlaAspProArgTrpSerCysLeuGlyGlySerArgThrGlu 80
 Db 458 -----GGTGGAAACCAACTAAT 475

Qy 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThr 100
 Db 476 AATGAGCGGAATTTTCTGTACGGTCTGCTATTTTGGCTACTCATCTGGAGAACGACG 535

Qy 101 ValSerSerGluLysValValArgValValLeuValGlnAlaAlaLeuValLysArg 120
 Db 536 ATGACATCGAACAAGATGCTATGATGTGCTTTTGAAGCAGCAGCCTTGTGAAGAGG 595

Qy 121 GlnLeuArgSerThrAspAspLeuGluValLysProAspIleValProGlyAsnLeu 140
 Db 596 CAACTGAGATCTACCAATAGATTGAAATGAAAGCCGGAATATACCTATTTCCGGGAATTTG 655

Qy 141 GlyLeuLeuSerGluAlaValArgAspArgCysGlyGluValCysAlaGluValArgThr 160

Db 656 GGCCTGTGAGTAGACATATGATAGCTGTGCGAAGTATGTCAGAGTATGCAAGACG 715
 Qy 161 PheTrpLeuGlyThrLysLeuMetThrProGluArgArgValAlaIleTpaAlaIleTyr 180
 Db 716 TTTAACTTAAAGAACTATGTCTTAATGACTCCGAGAGAAAGAGGCTATCTGGCAATATAT 775

Qy 181 ValTrpCysArgArgTrpAspGluLeuValAspGlyProAsnAlaSerHisIleThrPro 200
 Db 776 GTATGCGCAAGAAACAGATGAACTTGTGATGCGCCAAACCATATATATTAACCCG 835

Qy 201 GlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAsp 220
 Db 836 GCAGCCTTAATATGTGTGGGAAATAGGCTGAAAGATTTTCAATAGCGCCCAATTTGAC 895

Qy 221 MetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPhe 240
 Db 896 ATGCTCGATGCTGTGTGTGCGATACAGTTTCTAATCTTCAAGTTGATTCAGCCATTC 955

Qy 241 ArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTrpLysThrPheAsp 260
 Db 956 AGAGATATGATTTGAAGAAATGCGTATGCACTTGAGAAATCGAGATACAAAACCTTGAC 1015

Qy 261 GlnLeuTrpLeuTrpCysTrpTrpValAlaGlyThrValGlyLeuMetSerValProVal 280
 Db 1016 GAACATATACCTTATATTGTATTATGTTGCTGTGATACGGTGGGTGATGAGTGTCCAAAT 1075

Qy 281 MetGlyIleAlaProGluSerLysValAlaThrThrGluSerValTyrAsnAlaAlaLeuAla 300
 Db 1076 ATGGATATGCCCCCTGATCAATCAAGGCAACAGAGCGTATATATATATATGCTTGGCT 1135

Qy 301 LeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArg 320
 Db 1136 CTGGGATTCGCAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1195

Qy 321 GlyArgValTrpLeuProGluAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle 340
 Db 1196 GGAAGATCTACTTGTGCTCAAGATGAATAGCACAGCAGAGTCTATCCGATGAAGATATA 1255

Qy 341 PheAlaGlyArgValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAla 360
 Db 1256 TTGCTGGAAGGGTGACCGATTAATGAGAAATCTTTATGAGAAACCAATACATAGGGCA 1315

Qy 361 ArgLysPhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrp 380
 Db 1316 AGAAAGTCTTTGATGAGCGCAGAAAGCGCTGACAGAAATGAGCTACGTAAGTAAATTC 1375

Qy 381 ProValLeuThrAlaLeuLeuLeuTrpArgLysIleLeuAspGluIleGluAlaAsnAsp 400
 Db 1376 CCGTATGGGCACTTTGCTGTGACCGCAAAATATATGATGATGAAAGCAATGAC 1435

Qy 401 TyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuPro 420
 Db 1436 TACAACAACCTTCAACAAGAGCAATATGATGACAAACCAAGAAATGATGATTCATTA 1495

Qy 421 IleAlaTyrAlaLysSerLeuValProProAsnArgThrSerSer 435
 Db 1496 ATTGCATATGCAAAATCTCTTGTGCTCTTCAACAAAATCTGCTCT 1540

RESULT 4
 A68204 1239 bp DNA linear PAT 06-MAY-1999
 LOCUS A68204
 DEFINITION Sequence 2 from Patent WO9746690.
 ACCESSION A68204
 VERSION A68204.1 GI:4759372
 KEYWORDS
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 REFERENCE 1 (bases 1 to 1239)
 AUTHORS Drake,C.R., Bird,C.R. and Schuch,W.W.

TITLE ENHANCEMENT OF GENE EXPRESSION
JOURNAL Patent: WO 9746690-A 2 11-DEC-1997;
ZENECA LTD (GB)
FEATURES Location/Qualifiers
source 1..1239
/organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/db_xref="taxon:4081"
/clone="GTONS - PHYTOENE SYNTHASE GENE"

BASE COUNT 377 a 207 c 317 g 338 t
ORIGIN

Alignment Scores:
Pred. No.: 1,58e-141 Length: 1239
Score: 1750.00 Matches: 344
Percent Similarity: 86.84% Conservative: 32
Best Local Similarity: 79.45% Mismatches: 33
Query Match: 77.09% Indels: 24
DB: Gaps: 3

US-09-847-081B-2 (1-440) x A68204 (1-1239)

QY 3 MetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAnglyThrGly 22
DB 1 ATGCTGTGGCTTGTATGAGGTGTTCTCTCT--TGACGCTCTCAATGGACAGT 57
QY 23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42
DB 58 TTCATGGAATCACTCCGGAGGAGAACCGTTTTCGATTCACTG-----AGG 105
QY 43 AspArgAsnLeuMetTrpAsnGlyArgGlyLeuValGlyArgGlnArgTrpAsn 62
DB 106 CATGAAATTTGGTGTCCATGAGAGATCAATGATAGAGT----- 144
QY 63 GlySerLeuIleAlaAspProArgTrpSerCysLeuGlyGlySerArgThrGlyGly 82
DB 145 -----GGTGGAAAGCAATCAATATATGGA 168
QY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSer 102
DB 169 CGAATATTTCTGTAGCGTGTCTATTTGGCTACCTCCATCGAAGACGAGAGAGACA 228
QY 103 SerGluLeuValValTrpAspValValLeuValGlnAlaAlaLeuValValSerGlnLeu 122
DB 229 TCGAAGACAGTGTCTATGATGTGTTTACGACAGGACCTTGTGTGAAGGCAACTG 288
QY 123 ArgSerThrAspAspLeuGluValValProAspIleValValProGlyAsnLeuGlyLeu 142
DB 289 AGATCTACCAATAGTTAGAGTGAAGCCGAGATATCACTATCCGGGAAATTTGGGCTTG 348
QY 143 LeuSerGluAlaIleTrpAspArgCysGlyGluValCysAlaGluTrpAlaIleThrPheTrp 162
DB 349 TTGAGTGAAGCATATATAGTGTGTGAGATGTGCGAGATGCCAAGAGAGTTTAAAC 408
QY 163 LeuGlyThrIleLeuMetThrProGluArgArgAlaIleTrpAlaIleTrpValTrp 182
DB 409 TTAGGAACATATGCTATATGACTCCCGAGAGAGAGAGGCTATCTGGCAATATATGATG 468
QY 183 CysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAla 202
DB 469 TCGAGAGAGAGAGATGATGATGTTGATGCGCCCAAGCATATATATCCCGGAGAGCC 528
QY 203 LeuAspArgTrpGluTrpArgLeuGluValIlePheSerGlyArgProPheAspMetLeu 222
DB 529 TTAGATAGGAGGAGAAATAGGCTGAGAGAGATTTCAATGGGCGCATTTGACATGCTC 588
QY 223 AspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAsp 242
DB 589 GAGGAGGCTTTGTCCCATACAGTTTCACTTCCAGTTGATATTTGACCATTCACAGAT 648
QY 243 MetIleGluGlyMetArgMetAspLeuTrpValSerArgTrpValSerThrPheAspGluLeu 262
DB 649 ATGATTTGAAGAGATGCGTATGACTTGAGAAATTCAGATACAAAACTTCGAGAACTA 708

QY 263 TyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282
DB 709 TACCTTTATGTATATATGCTTCTGCTGACGCTGGGCTTGATAGAGTTCATTTATGGGT 768
QY 283 IleAlaProGluSerIleValThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGly 302
DB 769 ATCGCCCTTGATCAAGAGCAACACAGAGAGCGTATATATGCTTGGCTCGGGG 828
QY 303 LeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArg 322
DB 829 ATCGCAATCAATTTACTCACTCACTCACTGAGATGTTGAGAGAGATCCAGAGAGAGA 888
QY 323 ValTyrLeuProGluAspGluLeuValAlaGlnAlaGlyLeuSerAspGluAspIlePheAla 342
DB 889 GTCCTCTTCCCTCAAGATGAAATTTACACAGAGGCTCTATCCGATGAGATATATTTGCT 948
QY 343 GlyArgValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaArgLys 362
DB 949 GGAAGGGTGACCGATTAATGAGAGATCTTTATGAGAAACAAATACATAGGGCAAGAAAG 1008
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DB 1009 TTCTTTGATGAGCAGAGAGAGAGAGCGCTGACAGATTTGACTCAGCTAGATGATTCCTGTA 1068
QY 383 LeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsn 402
DB 1069 TGGGATCTCTTGTGCTTTGTACCGCAAAATCTAGATGAGATTGAGGCCAATACTACAC 1128
QY 403 AsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuProIleAla 422
DB 1129 AACTTCACAAAGAGAGCATATGTGAGCAATCAAAAGAGTTGATTCATTTACATTGCA 1188
QY 423 TyrAlaLysSerLeuValProProAsnArgThrSerSer 435
DB 1189 TATGCAAAATCTTGTGCTCTCTACAAAACCTGCTCT 1227

RESULT 5
AR156064 1239 bp DNA linear PAT 08-AUG-2001
LOCUS AR156064
DEFINITION Sequence 2 from patent US 6239331.
ACCESSION AR156064
VERSION AR156064.1 GI:15124117
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1239)
AUTHORS Drake, C. Rachel., Bird, C. Roger. and Schuch, W. Walter.
TITLE Enhancement of tomato phytoene synthase gene expression with a modified DNA
JOURNAL Patent: US 6239331-A 2 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..1239
/organism="unknown"
BASE COUNT 377 a 207 c 317 g 338 t
ORIGIN

Alignment Scores:
Pred. No.: 1,58e-141 Length: 1239
Score: 1750.00 Matches: 344
Percent Similarity: 86.84% Conservative: 32
Best Local Similarity: 79.45% Mismatches: 33
Query Match: 77.09% Indels: 24
DB: Gaps: 3

US-09-847-081B-2 (1-440) x AR156064 (1-1239)

QY 3 MetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAnglyThrGly 22
DB 1 ATGCTGTGGCTTGTATGAGGTGTTCTCTCT--TGACGCTCTCAATGGACAGT 57
QY 23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42

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Db      58  TTTCATGATCAGTCCGGAGGAAACCGTTTTCATGATC-----AGG 105
Oy      43  AspArganLeuMetTTPaenGlyArgGlyLeuValArgGlnArgTTPaenphe 62
Db      106  CATAGAAATTTGGTCCATGAGAAATCAATAGAGT----- 144
Oy      63  GlySerLeuLeaAspProArgTyrSerCysLeuGlyGlySerArgThrGlyLeuGly 82
Db      145  -----GGTGAAGACCAATCAATATATGA 168
Oy      83  SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGlyMetThrValSer 102
Db      169  CGAAATTTTCGTGCGCTGCTATTGCTTTCCTCATCTCGAGAACGCGCATGACA 228
Oy      103  SerGlyLeuValTyrAspValValLeuGlyGlnAlaLeuValLeuArgGlnLeu 122
Db      229  TCGGAACAGATGCTATGATGATGCTTTTGAAGCGAGCGCTTGTGAAGGCGACTG 288
Oy      123  ArgSerThrAspAspLeuGlyValAlaYsProAspIleValProGlyAsnLeuGlyLeu 142
Db      289  AGATTACCAATGATTTAGAGTGAAGCCGATATACCATTCGCGGAATTTGGGCTTG 348
Oy      143  LeuSerGlyAlaTyrAspArgCysGlyGlyValCysAlaGlyTyrAlaLysThrPheTyr 162
Db      349  TTGAGTGAAGCATATGATGATGCTGATGATGATGATGATGATGATGATGATGATG 408
Oy      163  LeuGlyThrLysLeuMetThrProGlyArgArgAlaIleThrAlaIleTyrValTyr 182
Db      409  TTAGAACTATGCTAATATGATGATGATGATGATGATGATGATGATGATGATGATG 468
Oy      183  CysArgGlyThrAspGlyLeuValAlaAspGlyProAsnAlaSerHisIleThrProGlnAla 202
Db      469  TCGCAAGAAACAGATGAACTGCTTGAATGCGCCAAACGATCATATATATATATATAT 528
Oy      203  LeuAspArgTyrGlyThrArgLeuGlyLeuAspIlePheSerGlyArgProPheAspMetLeu 222
Db      529  TTAGATAGTGGGAAATAGGCTAGAGATGATGATGATGATGATGATGATGATGATG 588
Oy      223  AspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAsp 242
Db      589  GATGCTGCTTGTGCGATACAGTTTCACTTCCAGTGTATTCACCCATTCAGAAAT 648
Oy      243  MetIleGlyGlyMetArgMetAspLeuTyrLysSerArgTyrLysThrPheAspGlyLeu 262
Db      649  ATGATTGAAGAAATCGATGACTTGAAGAAATGAAATGAAATGAAATGAAATGAAATG 708
Oy      263  TTYLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282
Db      709  TACCTTATGCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
Oy      283  IleAlaProGlySerLeuValAlaThrThrGlySerValTyrAsnAlaAlaLeuAlaLeuGly 302
Db      769  ATCGCCCTGATCAAGGCAACAGCAAGCGATATATATGCTGCTGCTGCTGCTGCTG 828
Oy      303  LeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGlyAspAlaArgGlyArg 322
Db      829  ATCGAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 888
Oy      323  ValTyrLeuProGlnAspGlyLeuAlaGlnAlaGlyLeuSerAspGlyAspIlePheAla 342
Db      889  GTCATCTGCTCAAGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTA 948
Oy      343  GlyArgValThrAspLysTyrArgAsnMetLeuLysGlnIleGlnArgAlaArgLys 362
Db      949  GGAAGGCGACCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008
Oy      363  PhePheAspGlySerGlyLeuGlyValThrGlyLeuAspSerAlaSerArgTyrProVal 382
Db      1009  TTCTTTATGAGGCGAGAAAGGCGTGAACAGATTAATTAATTAATTAATTAATTA 1068
Oy      383  LeuThrAlaLeuLeuTyrArgLysIleLeuAspGlyIleGlyAlaAsnAspTyrAsn 402

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Db      1069  TGGGCATCTTGGTCTTGATCCGCAAAATCAATGATGATGAAAGCAATGACTACAC 1128
Oy      403  AspPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuProIleAla 422
Db      1129  AACTTCACAAAGAGAGATATGAGCAAAATCAAAAGAAATGATGATGATGATGATG 1188
Oy      423  TyrAlaLysSerLeuValProProAsnArgThrSerSer 435
Db      1189  TATGCAAAATCTTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227

RESULT 6
BD005486
LOCUS      1239 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Enhancement of gene expression.
ACCESSION  BD005486
VERSION     BD005486.1 GI:18633857
KEYWORDS    JP 2001501810-A/2.
SOURCE      Lycopersicon esculentum (tomato)
ORGANISM    Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 1239)
Drake, C.R., Bird, C.R. and Schuch, W.W.
Enhancement of gene expression
Patent: JP 2001501810-A 2 13-FEB-2001;
ZENBECA LTD

COMMENT
OS      Lycopersicon esculentum (tomato)
PN      JP 2001501810-A/2
PD      13-FEB-2001
PF      23-MAY-1997 JP 1998500302
PR      07-JUN-1996 GB 9611981.3
PI      CAROLINE RACHEL DRAKE, COLIN ROGER BIRD, WOLFGANG WALTER SCHUCH
PC      C12N15/67, C12N15/82, C12N15/29, C07K14/415
CC      Strandedness: Double;
CC      Topology: Linear;
FH      Key
FT      source
FT      location/Qualifiers
FT      1..1239
FT      /organism='Lycopersicon esculentum (tomato)',
FT      location/Qualifiers
FT      1..1239
FT      /organism='Lycopersicon esculentum'
FT      /mol_type='genomic DNA'
FT      /db_xref='taxon:4081'

BASE COUNT      377 a 207 c 317 g 338 t

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ACCESSION  A68203
VERSION     A68203.1 GI:4759371
KEYWORDS   SOURCE
ORGANISM   unidentified
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REFERENCE   1 (bases 1 to 1239)
AUTHORS    Drake, C.R., Bird, C.R. and Schuch, W.W.
TITLE       ENHANCEMENT OF GENE EXPRESSION
JOURNAL     Patent: WO 9746690-A 1 11-DEC-1997;
            ZENCA LTD (GB)
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BASE COUNT 343 a 247 c 320 g 329 t
ORIGIN
Alignment Scores:
Pred. No.: 5,19e-141      Length: 1239
Score: 1744.00           Matches: 343
Percent Similarity: 86.61%      Conservative: 32
Best Local Similarity: 79.21%      Mismatches: 34
Query Match: 76.83%           Indels: 24
DB: 6                      Gaps: 3
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Db      58 TTTATGAGAGGTGTAGAGAAAGGTATATGATTTCTTCAGACATTTCT-----CGT 105
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Qy 203 LeuaspargtrpGluThrArgLeuGluaspIlepheserGlyArgProphaspMetLeu 222
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 Db 649 ATGATCGAGGCGATAGAAATGATCTTCGTAAAGTCTCGTTATTAAGATTTGATGATG 708
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 Db 1069 TGGGCGACCTTGCTCTATAGAAAGATTTTGGAGCAATTCAGAGCTATATATAT 1128
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 LOCUS DEFINITION Sequence 1 from patent US 6239331.
 ACCESSION ARI56063
 VERSION ARI56063.1 GI:15124116
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1239)
 AUTHORS Drake, C. Rachel, W. Bird, C. Roger, and Schuch, W. Walter.
 TITLE Enhancement of tomato phytoene synthase gene expression with a modified DNA
 JOURNAL Patent: US 6239331-A 1 29-MAY-2001;
 FEATURES Location/Qualifiers
 SOURCE 1..1239
 BASE COUNT 343 a 247 c 320 g 329 t
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 Alignment Scores: 5.19e-141 Length: 1239
 Score: 1744.00 Matches: 343
 Percent Similarity: 86.61% Conservative: 32

Best Local Similarity: 79.21% Mismatches: 34
 Query Match: 76.83% Indels: 24
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 US-09-847-081b-2 (1-440) x ARI56063 (1-1239)
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 Qy 23 LeuLeuAspSerValAlaGluGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42
 Db 58 TTTATGAGAGGTGTGAGAGAGGTAATGATTTCTTCAAGATTTCT-----CGT 105
 Qy 43 AspArgAsnLeuMetTyrAsnGlyArgIleLysLysGlyGlyArgGlnArgTyrPasnPhe 62
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 Db 589 GACGAGACCTTAGAGCACTGTGAGCAATTTCCCTGGACATCCACTTTTCGGGAC 648
 Qy 243 MetIleGluGlyMetArgMetAspLeuThrPlySerArgGlyTyrIlePheaspGluLeu 262
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 Qy 263 TyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282
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 LOCUS BD005485 Enhancement of gene expression.
 DEFINITION BD005485
 ACCESSION BD005485.1 GI:18633856
 VERSION JP 2001501810-A/1.
 KEYWORDS unclassified
 SOURCE unclassified
 ORGANISM unclassified
 unclassified.
 1 (bases 1 to 1239)
 REFERENCE Drake, C.R., Bird, C.R. and Schuch, W.W.
 AUTHORS Enhancement of gene expression
 TITLE Patent: JP 2001501810-A 1 13-FEB-2001;
 JOURNAL ZENCA LTD
 COMMENT OS Unidentified
 PN JP 2001501810-A/1
 PD 13-FEB-2001
 PE 23-MAY-1997 JP 1998500302
 PR 07-JUN-1996 GB 9611981.3
 PI CAROLINE RACHEL DRAKE, COLIN ROGER BIRD, WOLFGANG WALTER SCHUCH
 PC C12N15/67, C12N15/82, C12N15/29, C07K14/415
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BASE COUNT 343 a 247 c 320 g 329 t
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Alignment Scores:
 Pred. No.: 5.19e-141 Length: 1239
 Score: 1744.00 Matches: 343
 Percent Similarity: 86.61% Conservative: 32
 Best Local Similarity: 79.21% Mismatches: 34
 Query Match: 76.83% Indels: 24
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US-09-847-081b-2 (1-440) x BD005485 (1-1239)

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 QY 63 GlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluLysGly 82
 Db 145 -----GGAGGTAACAGACAAACACCGT 168
 QY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSer 102
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 Db 649 ATGATCGAGGGCATAGATGATCTTGTAACTCTGTTAAAGATTTTGTATAGTTG 708
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 Db 709 TATTTGTACTCTACTACGTGGCAGAACCGTGGGCTTATGTCACTGCTCATATGAGGA 768
 QY 283 IleAlaProGluSerLysValIleThrGluSerValTyrAsnAlaIleLeuAlaLeuGly 302
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 QY 363 PhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrpProVal 382
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QY	403	AanbepthrragaxaialatyvaSerisyProlyslvlsleuLeThleuProlla1a	422
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DEFINITION	Tomato fruit ripening specific mRNA.		
ACCESSION	Y00521		
VERSION	Y00521.1		
KEYWORDS	GI:19340		
SOURCE	unidentified reading frame.		
ORGANISM	Lycopersicon esculentum (tomato)		
REFERENCE	Lycopersicon esculentum		
AUTHORS	Eukaryota; Vitridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
TITLE	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
JOURNAL	Asteridae; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.		
MEDLINE	1 Ray,J., Bird,C., Maunders,M., Grierson,D. and Schuch,W.		
PUBMED	Sequence of PTOM5, a ripening related cDNA from tomato		
REFERENCE	Nucleic Acids Res. 15 (24), 10587 (1987)		
AUTHORS	88096591		
TITLE	3697097		
JOURNAL	2 (bases 1 to 1614)		
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ORIGIN			470 t
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Best Local Similarity:	78.64%	Mismatches:	36
Query Match:	76.34%	Indels:	27
DB:	8	Gaps:	4

US-03-847-081B-2 (1-440) x LER1PE (1-1614)

QY	1	MetSerMetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGly	20
DB	195	CTCGAATGTCGTGTGCTCTGTGTATGGGTGTTCTCTCT--TGTGACGTCTCAATGGG	251
QY	21	ThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerCArgPheLeu	40
DB	252	ACAAAGTTTCATGAGAAATCATGCCGAGAGGAAAACCGTGTGTTTATTCATTCACG-----	302
QY	41	AlaArgAspArgAsnLeuMetTrpAsnGlyArgGlyLeuGlySerGlyGlyArgGlnArgTrp	60
DB	303	---AGGCATAGCAATTTGCTGCTCCATAGAGATCATTAAGGT-----	344
QY	61	AsnPheGlySerLeuLeuAlaAspProArgTrpSerCysLeuGlyGlySerArgThrGlu	80
DB	345	-----GGTGGAAACCAACTAAT--:::	362
QY	81	LySGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThr	100
DB	363	AATGACCGAAATTTTCTGACGGCTGTCATTTTGGCTACTCCATCTGGAGAACGGACG	422
QY	101	ValSerSerGluGlyValValTrpAspValValLeuGlyGlnAlaLeuValLysArg	120
DB	423	ATGACATCGGAACGATGTCTATGATGTGTTTGGACGACGACGCTTGTGTGAAGAG	482
QY	121	GlnLeuArgSerThrAspAspLeuGluValLysProAspIleValValProGlyAsnLeu	140
DB	483	CACTGACATCTCAACCAATGAGTATGAAATGGAACGGGATATACCTATCCGGGGAATTTG	542
QY	141	GlyLeuLeuSerGluAlaTrpAspArgCysGlyGlyValCysAlaGluTrpAlaLysThr	160
DB	543	GCGTTGTTGAATGAAGCATATGATAGGTGTGTAAGTATGTGCAGATATGCAAAAGACG	602
QY	161	PheTrpLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIleTrp	180
DB	603	TTTAACCTTAGAATCTATGCTATTAATCTCCAGAGAGAAAGGCTATCTGGCAATATAT	662
QY	181	ValTrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrPro	200
DB	663	GTAAGGTGCAGAAAGACGATGAACCTTGATGGCCCAACGCATCATATATTAACCCG	722
QY	201	GlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAsp	220
DB	723	GCAGGCTTAGATAGGTGGGAAATAGGCTAGAGATGTTTTCATATGGCGGCACATTGAC	782
QY	221	MetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPhe	240
DB	783	ATGCTCGATGGTGCCTTTGTCCGATACAGATTTCTAACTTCCAGTTGATATTCAGCATTC	842
QY	241	ArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTrpLysThrPheAsp	260
DB	843	AGAGTATGATTTGAAGAGATCGATATGACCTTGAGAAAATGAGATACAAAACCTTGAC	902
QY	261	GluLeuTrpLeuTrpCysTrpTrpValAlaGlyThrValGlyLeuMetSerValProVal	280
DB	903	GAACATATCTCTTATTTGTTATTAATGCTGTGTCGCTGGTGGGTGATGAGGTTCCAAATT	962
QY	281	MetGlyIleAlaProGluSerLysAlaThrThrGluSerValTrpAsnAlaAlaLeuAla	300
DB	963	ATGGGTATCGCCCTCGAATCAAGGCAACACAGAGACGATATATTAAGCTGTGGCTTGGCT	1022
QY	301	LeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArg	320
DB	1023	CTGGGGATCGCAATCAATTATCTACATCTCAGAGATGTTGGAGAAAGATGCCGAAGA	1082
QY	321	GlyArgValTrpLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle	340
DB	1083	GGAAGAGTCTACTTGCCCTCAAGATCAATTATTCACAGGACGCTATCTCGATGAAGATATA	1142
QY	341	PheAlaGlyArgValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAla	360
DB	1143	TTTGTCTGAAGAGGTGACCGATTAATGTGGAATCTTTATGAAGAAACAATATCATATGGGCA	1202


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QY      361 ArgLysPhePheAspGluSerGluValThrGluLeuAspSerAlaSerArgTrp 380
Db      1203 AGAAGATTCTTGATGAGCAGAGAAAGCGTGACGAATGAGCTCAGCTAGTATATTC 1262
QY      381 ProValLeuThrAlaLeuLeuLeuValArgLysIleLeuAspGluIleGluAlaAsnAP 400
Db      1263 CCTGATGGGCACTTTGGTCTTGATCCGCAAAATCTAGATGAGATTGACCAATGAC 1322
QY      401 TyrAsnAspPheThrArgTrgAlaTyrValSerLysProLys-LysLeuLeuThrLeuP 420
Db      1323 TACACAACTTCACCAAGAGACATATGAGCAAAATCAAGCAAGTGAATTCATTACC 1382
QY      420 oilealaTyrAlaLysSerLeuValProProAsnArgTrnSerSerProLeuAlaLys 439
Db      1383 TATTGATATGCAAATCTCTTGCTCTCT-----ACAAAATGCTCTCTTCAA 1434

RESULT 11
LOCUS      A21360      1646 bp      mRNA      linear      PAT 06-JUN-1994
DEFINITION L.esculentum pTOM5 mRNA.
ACCESSION  A21360
VERSION     A21360.1 GI:512395
KEYWORDS
SOURCE      Lycopersicon esculentum (tomato)
ORGANISM    Lycopersicon esculentum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 1646)

REFERENCE   1
  AUTHORS   DNA, CONSTRUCTS, CELLS AND PLANTS DERIVED THEREFROM
  TITLE     Patent: WO 9109128-A 1 27-JUN-1991.
  JOURNAL   Location/Qualifiers
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BASE COUNT 529 a      249 c      388 g      480 t
ORIGIN
polyA_site
/gene="pTOM5"

Alignment Scores:
Pred. No.:      8, 13e-140      Length:      1646
Score:          1732.00      Matches:      346
Percent Similarity: 85.68%      Conservative: 31
Best Local Similarity: 78.64%      Mismatches: 36
Query Match:     76.30%      Indels:      27
DB:             6      Gaps:      4

US-09-847-081B-2 (1-440) x A21360 (1-1646)
QY      1 MetSerMetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAngly 20
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Db      195 CTCAGAAATGCTGTTGCTTGTATGCGTGTGTTCTCTCT---TGTAGCGTCAAAATGGG 251
QY      21 ThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu 40
Db      252 ACAAGTTTCATGAAATCAGTCCGGAGGGGAAACCGTTTTTGTGATTCAACG----- 302
QY      41 AlaArgAspArgAsnLeuMetTrpPasnGlyArgIleLysLysGlyValArgGlnArgTrp 60
Db      303 ---AGGCATAGGAATTTGGTGTCCAAATAGAGAAATCAATAGACGT----- 344
QY      61 AsnPheGlySerLeuIleAlaAspProArgTrpSerCysLeuGlyGlySerArgTrpGlu 80
Db      345 -----GGTGAAGAACCAACTAAT 362
QY      81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetTrp 100
Db      363 AATGACGGAATTTTGTGACGTCTATTTGGCTACTCTCATCTCGAATCGGAAGGAGCG 422
QY      101 ValSerSerGluLysLeuValTyrAspValValIleuLysGlnAlaAlaLeuValLysArg 120
Db      423 ATGACATCGGAACACATGCTCATATGATGTTGTAGACGACGACCTTGSTGAAGAG 482
QY      121 GlnLeuArgSerThrAspAspLeuGluValLysProAspIleValProGlyAsnLeu 140
Db      483 CAACGAGATCTACCAATGAGTTAGAGTGAAGCCGGAATATCTATTCGGGGAATTGG 542
QY      141 GlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysTrp 160
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QY      161 PheTyrLeuGlyThrLysLeuMetThrProGluArgArgArgAlaIleTrpAlaLysTrp 180
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QY      181 ValTrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrPro 200
Db      663 GTATGTCGACAGAAACAGATGAACTTGTGTATGSCCAAAAGCATATATTTACCCGG 722
QY      201 GlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAsp 220
Db      723 GCAGCTTAGATGATGGTGGGAAATAGGCTAGAGATGTTTCAAGGGCGGCATTGTGAC 782
QY      221 MetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPhe 240
Db      783 ATGCTCGATGCGCTTGTTCATACATGCTTTCATCTTCAGATTATTCAGCCATTTC 842
QY      241 ArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAsp 260
Db      843 AGAGATATGATTGAAGAGATGGTATGACTTGAAAMAATGAGATACAAAACCTTCGAC 902
QY      261 GlyLeuValTrpLeuValCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProVal 280
Db      903 GAACATATACCTTATATGTTATATGTTCTGCTGATAGGTTGGTGTATGATGATTCCTCAATT 962
QY      281 MetGlyIleAlaProGlySerLysValAlaThrTrpGluSerValTyrAsnAlaAlaLeuAla 300
Db      963 ATGGATATCGCCCTCAATCAAGGACCAACAGAGAGCGTATATATATGCTGCTTGGCT 1022
QY      301 LeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArg 320
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QY      321 GlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle 340
Db      1083 GGAAAGCTCTACTTGCCTCAAGATGAATTAGACAGCGAGGCTATCCGATTAATAATATA 1142
QY      341 PheAlaGlyArgValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAla 360
Db      1143 TTTGCTGAAGGGGTACCGATTAATGAGAAATCTTTATGAGAAACCAATATCATATGCGGA 1202
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OY		381	ProValLeuThrAlaIleuLeuMetTyrArgLysIleLeuAspGlnIleGluAlaAsnsp	400
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OY		401	TyrAsnAsnPhetHrArgRsnAlaTyrValSerLysProLys-LysLeuLeuThrLeuPr	420
Dd		1323	TACAACAACCTTCACAAAGAAGACATATATGTAGAACAAATCAAAGCAGATTGATTCACC	1382
OY		420	GlleAlaTyrAlaLysSerLeuValProProAsnArghTrhSerSerProLeuAlaLys	439
Dd		1383	TATTGCATATAGCAAAAATCTTTGTGCCCTCT-----ACAAAACTGCTCTTCCAAA	1434
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LOCUS	AR007503	1646 bp	DNA	linear
DEFINITION	Sequence 2 from patent US 5750865.			PAT 04-DEC-1998
ACCESSION	AR007503			
VERSION	AR007503.1	GI:3966987		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1646)			
TITLE	Bird,C.Roger., Grierson,D. and Schuch,W.Walter. Process for modifying the production of carotenoids in plants, and DNA constructs and cells therefor			
JOURNAL	Patent: US 5750865-A 2.12-MAY-1990;			
FEATURES	Location/Qualifiers			
SOURCE	1..1646			
BASE COUNT	529 a 249 c 388 g 480 t			
ORIGIN	/Organism="unknown"			
Alignment Scores:				
Pred. No.:	8.13e-140	Length:	1646	
Score:	1732.00	Matches:	346	
Percent Similarity:	85.68%	Conservative:	31	
Best Local Similarity:	78.64%	Mismatches:	36	
Query Match:	76.30%	Indels:	27	
DB:	6	Gaps:	4	
US-09-847-081B-2 (1-440) x AR007503 (1-1646)				
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OY		21	ThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu	40
Dd		252	ACAACTTTCATCGAATCACTCCGGAGGGAACCCGTTTTTTTGATTCATCG-----	302
OY		41	AlaArgAspArgAsnLeuMetTrrpsanGlyArgGlyLysGlyGlyArgGlnArgTrp	60
Dd		303	--AGGCATAGGAATTTGGTGTCCATAGAAATCAATAGAGGT-----	344
OY		61	AsnPhgJySerLeuIleAlaAspProArgrTrrSerCySleuGlyGlySerArgThrGlu	80
Dd		345	-----GGTGAAGAACTAAT	362
OY		81	LysGlySerTrhPssServAlcInserSerLeuValAlaSerProAlGlyGluMetThr	100
Dd		363	AATGACGGAAMATTTCTGTACGGCTCGTATTTTGGCTACTCCATCTGGAGAACGGACG	422
OY		101	ValSerSerGluLysLeuValTrrpsPvalValLeuLysGlnAlaIleValLysArg	120
Dd		423	ATGACATCGGAACAGATGCTCTATATATGTGTGTGAGCGAGCACCTGTGTGAAGAG	482
OY		121	GlnLeuArgSerTrhAspAspleuGluValLysProAspIleValAlaProGlyAsnLeu	140
Dd		483	CAACTGAGATCTCAACATAGTAGTTAGAGAGGAACCGGATATATCCATTCGGGGAAATTTG	542
OY		141	GlyLeuLeuSerGluAlaTyrAspArgCySglyGluValCysAlaGluTrrAlaLysThr	160

Db	543	GCCTTGTGATGAGATGATGATAGGTGTGCTGAATATCTGCAGAGTATGCAAAACG	602
Qy	161	PheTyrLeuGlyThrTyrSLeuMetThrProGluArgArgAlaIleTTPAlaIleTyr	180
Db	603	TTTAACTTAGAAGCTAATAGTAAATGACTCCGAGAGAAAGAGGCTATCTGGGCAATATAT	662
Qy	181	ValTProValArgArgThrArgPyluLeuValAspGlyProAsnAlaSerHisIleThrPro	200
Db	663	GTAATGTCAGAAACAGATGAATCTTGATGATGGCCCAACGATATATATTAACCCG	722
Qy	201	GlnAlaLeuAspArgTTPGluThrArgLeuGluAspIlePheSerGlyArgProPheAsp	220
Db	723	GCACCTTAGATAGTGTGGAAAAATAGGCTGAAGATGTTTTCATAGGGCGGCCATTTGCAC	782
Qy	221	MetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPhe	240
Db	783	ATGCTCATAGGTGCTTTGTCCGATACAGTTTCTAACTTCCAGTTGATATTCAGCCATTC	842
Qy	241	ArgAspMetIleGluGlyMetArgMetAspLeuThrPyluSerArgTyrTyrThrPheAsp	260
Db	843	AGAAATATGATGAAAGAAATGCGATGAGCTTGAGAAATCGAATACAAAACTTGAC	902
Qy	261	GluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProVal	280
Db	903	GAACTATACCTTATTTGTATTAATGTTGCTGTRCGGTTGGGTTGATGAGGTTCACATT	962
Qy	281	MetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAla	300
Db	963	ATGGGTATCGCCCTGGAATCAAAAGCAACAACAGACGCTATATATATGCTGCTTGCGCT	1022
Qy	301	LeuGlyLeuAlaAsnGluLeuThrAsnIleLeuArgAspValGlyValAspAlaArgArg	320
Db	1023	CTGGGATTCGCAAAATCAATTAATCACTACATCACTCAGATGTGTGAGAAAGATGCCAAGA	1082
Qy	321	GlyArgValTyrLeuProGluAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle	340
Db	1083	GGAAGAGTCTACTTGCTCTCAAGATGAATTAGCACAGCGAGGTCTATCCGATGAAGATATA	1142
Qy	341	PheAlaGlyArgValThrAspLysTyrTPaArgAsnPheMetLysLysGlnIleGlnArgAla	360
Db	1143	TTTCTCGAAGCGGAGCAGCATTAATGAGATCTTTTATGAAGAAACAAATACATAGAGGCA	1202
Qy	361	ArgLysPhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTyrP	380
Db	1203	AGAAAGTCTTGTATGAGGCGAGAAAGCGGTGCACAAATTGACCTCAGTATGAGATTC	1262
Qy	381	ProValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAsp	400
Db	1263	CTGTATGGGCATCTTTGGTCTGTATACCGCAAAATACTAGATGAGATTGAAGCCAAATGAC	1322
Qy	401	TyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuP	420
Db	1323	TACAACAACCTTCACAAAAGAGCATATGTGAGCAAAACAAGCAAGTATGATTCATTCAC	1382
Qy	420	OllaAlaTyrAlaLysSerLeuValProProAsnArgThrSerSerProLeuAlaLys	439
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RESULT 13

LOCUS LERVYGTOMS 1355 bp mRNA linear PLN 02-AUG-1993

DEFINITION L.esculentum (xy mutant) GTOMS mRNA for mutant phytoene synthase.

VERSION X67144.1 GI:19346

KEYWORDS GTOMS gene; mutant; phytoene synthase.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum

REFERENCE 1 (bases 1 to 1355)

Frayer, R.G. and Grierson, D.

TITLE Identification and genetic analysis of normal and mutant phytoene synthase genes of tomato by sequencing, complementation and co-suppression

JOURNAL Plant Mol. Biol. 22 (4), 589-602 (1993)

MEDLINE 93344508

PUBMED 8343597

REFERENCE 2 (bases 1 to 1355)

AUTHORS Fray, R.G.

TITLE Direct Submission

JOURNAL Submitted (01-JUL-1992) R.G. Fray, University of Nottingham, School of Agriculture, Sutton Bonington, Loughborough, Leicestershire LE12 5RD, UK

FEATURES

source Location/Qualifiers

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Alignment Scores:

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Score: 1668.00 Matches: 329

Percent Similarity: 86.27% Conservative: 29

Best Local Similarity: 79.28% Mismatches: 33

Query Match: 73.48% Indels: 24

DB: 8 Gaps: 3

US-09-847-081b-2 (1-440) x LERRYGTOM5 (1-1355)

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QY 42 ArgAspArgAsnLeuMetTrpAsnGlyArgGlyLeuGlyGlyArgGlnArgTrpAsn 61

DB 111 AGGCATAGGAATTTGGTCCCAATGAGATCAATCAATAGAGGT----- 152

QY 62 PheGlySerLeuIleAlaAspProArgTrpSerCysLeuGlyGlySerArgThrGluLys 81

DB 153 -----GGTGGAAAGCAAACTAATAT 173

QY 82 GlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyLeuMetThrVal 101

DB 174 GGACGGAATTTTCTGTACGGCTGCTGATTTTGGCTACTCATCTGAGAAAGGACATG 233

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DB 234 ACATCGAACAGATGCTTATGATGTGGTTTGAGACGAGCGCTTGTAAGAGGACA 293

QY 122 LeuArgSerThrAspAspLeuGluValLysProAspIleValIleProGlyAsnLeuGly 141

DB 294 CTGAGATCTACCAATGAGATTGAGAGTGAAGCCGATATACCATTCGCGGGAATTTGGGC 353

QY 142 LeuLeuSerGluAlaTyrAspArgCysGlyGlyValGlyValAlaGlyTyrAlaLysThrPhe 161

DB 354 TTGTTGAGTGAAGCATATGATGATGCTGTGTGAGATGATGAGATGATGCAAGACGTTT 413

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DB 414 AACCTAGGAACATGCTATATGACTCCAGAGAAAGAGGCTATCTGGCAATATATGTA 473

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DB 474 TGGTCCAGAAAGACGATGAATCTTGTATGAGCCCAAGCATCATATATATCCCGGCA 533

QY 202 AlaLeuAspArgTrpGlyThrArgLeuGlyLysPheSerGlyArgProPheAspMet 221

DB 534 GCCTTAGATGAGTGGGAAATAGGCTAGAGATGTTTCAATGGCGGCATTGTGACATG 593

QY 222 LeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArg 241

DB 594 CTCGATGGTCTTGTTCGATACAGTTTCTTAACITTCAGATGAAATTCACGCAATTCAGA 653

QY 242 AspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGlu 261

DB 654 GATATGATGGAAGAAATCGTATGACCTTGGAAGAAATCGAAGATCAAAAACCTCCAGCAA 713

QY 262 LeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMet 281

DB 714 CTAATCCTTATTTGTTATTAATCTTCTGTCGCTGAGTGGTGTGATGAGTTCATTTATG 773

QY 282 GlyIleAlaProGluSerLeuAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeu 301

DB 774 GGTATCGCCCTGAAATCAAGGCAACACAGAGACCGATATATATGCTGCTTGGCTCTG 833

QY 302 GlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGly 321

DB 834 GGGATCGCAATCAATTAATTAATCACTACAGATGTTGGAAGAAATGCCGAAGAGCA 893

QY 322 ArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePhe 341

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DB 954 GCTGGAAGGCTGACCGATTAATGAGAAATCTTTATGAAAGAAACAAATCATGTGGCAAGA 1013

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DB 1074 GTATGGGACATCTTGTCTGTGAACGCAAAATATCATAGATGAGATGGAAGCCATGACTAC 1133

QY 402 AsnAsnPheThrArgArgAlaTyrTyrAlaSerLysProLysLysLeu 416

DB 1134 AACCACTTCACAAAGAGAGCATATGTGCAAAATCATATATGCTC 1178

RESULT 14

AF220218 1506 bp mRNA linear PLN 11-FEB-2000

DEFINITION Citrus unshiu phytoene synthase (Pey1) mRNA, complete cds.

ACCESSION AF220218

VERSION AF220218.1 GI:6959859

KEYWORDS

SOURCE Citrus unshiu
ORGANISM Citrus unshiu
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Sapindales; Rutaceae; Citrus.

REFERENCE 1 (bases 1 to 1506)
Kim, I.-J., Ko, K.-C., Kim, C.-S. and Chung, W.-I.
Isolation of a cDNA encoding phytoene synthase from Citrus unshiu
2 (bases 1 to 1506)

REFERENCE 2 (bases 1 to 1506)
Kim, I.-J., Ko, K.-C., Kim, C.-S. and Chung, W.-I.
Direct Submission
Submitted (30-Dec-1999) Biological Sciences, Korea Advanced Institute of Science and Technology, 373-1 Kusong-dong, Yuseong-gu, Taejeon 305-701, South Korea

FEATURES
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BASE COUNT 448 a 271 c 360 g 427 t

ORIGIN

Alignment Scores:
Pred. Nc: 9.9e-131 Length: 1506
Score: 1626.00 Matches: 327
Percent Similarity: 82.61% Conservat: 34
Best Local Similarity: 74.83% Mismatches: 64
Query Match: 71.63% Indels: 12
Gaps: 4

US-09-847-081b-2 (1-440) x AF220218 (1-1506)

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Db 109 AGCATGTCGTGTACATTCTGTGGGTGTATCACTCACTCAATGTCCATTTGCTTC 168
Oy 22 GluLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu 40
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Oy 41 --AAtArgAspArgAsnLeuMetTrpAsnGlyArgIleGly 56
Db 229 CAACATCAAAACCGGACCTGCTGTATTCTTAACTTCAAGCACTTAATTAATGTAAT 288
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RESULT 15
AB037975 1689 bp mRNA linear PLN 25-NOV-2000
DEFINITION Citrus unshiu mRNA for phytoene synthase, complete cds.
ACCESSION AB037975
VERSION AB037975.1 GI:11344506

KEYWORDS phytoene synthase.
SOURCE Citrus unshiu
ORGANISM Citrus unshiu
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Sapindales; Rutaceae; Citrus.
REFERENCE 1 (sites)
AUTHORS Ikoma,Y., Komatsu,A., Kita,M., Ogawa,K., Omura,M., Yano,M. and
Moriguchi,T.
TITLE Expression of a phytoene synthase gene and characteristic carotenoid
accumulation during citrus fruit development
JOURNAL Physiol. Plantarum 111, 232-238 (2001)
REFERENCE 2 (bases 1 to 1689)
AUTHORS Moriguchi,T.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-2000) Takaya Moriguchi, National Institute of
Fruit Tree Science, Department of Research Planning and
Coordination, 2-1 Fujimoto, Tsukuba, Ibaraki 305-8605, Japan
(E-mail: takaya@fruit.affrc.go.jp, Tel: 81-298-38-6416,
Fax: 81-298-38-6437)
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BASE COUNT 512 a 302 c 388 g 487 t
ORIGIN
Alignment Scores:
Pred. No.: 1,15e-130 Length: 1689
Score: 1626.00 Matches: 327
Percent Similarity: 82.61% Conservative: 34
Best Local Similarity: 74.83% Mismatches: 64
Query Match: 71.63% Indels: 12
DB: 8 Gaps: 4
US-09-847-081b-2 (1-440) x AB037975 (1-1689)
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DB 176 AGCAGTCTGTTACATTGCTGTGGTGTGATCACTCACTCAATTGCCAATTGCTTC 235
QY 22 GlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu 40
DB 236 GGGTTCGTCGATTGCTGAGAGAAAACAGGCTGTTTATTCATCAAGATTCTTTAC 295
QY 41 ---AlaArgAspArgAsnLeuMetTrpAsnGlyArgGlyLeuValys-----GlyGly 56
DB 236 CAACATCAAAACCCGACCTGCTGTATTATTTCTAAGCCTTAACAGATTATATATGTAAT 355
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DB 356 AAGCAGAGACGGAATTCATTATCTTATGATACAGATTGAGGACATCTTGC----- 406
QY 77 SerArgThrGluGlyGlySerThrPheSerValGlnSerSerLeuValAlaSerProAla 96
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DB 1358 ATTGAGGCAATGATTACAAACAATCTTCAAAAGAGCTTTATGTGATGAAGCCCAAGAG 1417
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Search completed: January 16, 2004, 08:00:26
Job time : 5065 secs

and is derived by analysis of the total score distribution.

SUMMARIES

Database : N_Geneseq_19Jun03:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed

SUMMARIES

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2	2143.5	94.4	1573	25	ABX13568	Tobacco phytoene s	
3	1826	80.4	1826	19	AAV03880	phytoene synthase	
4	1801	79.3	1712	24	AA166367	Nicotiana tabacum	
5	1799	79.3	1814	19	AAV03881	phytoene synthase	
6	1774	78.1	1951	19	AAV03878	phytoene synthase	
7	1762	77.6	1316	19	AAV03879	phytoene synthase	
8	1751	77.1	1591	17	AAQ93323	Melons, modified ph	
9	1744	76.8	1239	19	AAV17243	CDNA encoding a ph	
10	1737	76.5	1239	24	AAZ299482	Tomato phytoene sy	
11	1737	76.5	1239	24	AMD40272	Tomato fruit ripen	
12	1729	76.2	1456	12	AAO12495	Nucleic acid encod	
13	1595	70.3	2868	19	AAV16951	Nucleic acid encod	
14	1557	68.6	1921	19	AAV16949	Nucleic acid encod	
15	1542	67.9	1269	24	ABZ12924	Arabidopsis thalia	
16	1542	67.9	1566	21	AAAC4162	Arabidopsis thalia	
17	1542	67.9	1703	21	AAAC3140	Arabidopsis thalia	
18	1531	67.4	2085	19	AAV16948	Nucleic acid encod	
19	1523	67.1	1932	19	AAV16950	Nucleic acid encod	
20	1514	66.7	2585	23	ABL41600	Nucleic acid encod	
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22	1393	61.4	1397	21	AAZ29139	Nucleotide sequenc	
23	1252.5	55.2	1448	21	AAZ29145	Soybean phytoene s	
24	1078	47.5	1021	21	AAZ29146	Corn phytoene synt	
25	1033.5	45.5	3485	13	AAO28211	Wheat phytoene syn	
26	1033	43.5	992	21	AAZ28144	Fragment of GROM5	
27	992	43.7	1060	21	AAZ28143	Soybean phytoene s	
28	781.5	34.4	888	21	AAZ29142	Rice phytoene synt	
29	511	22.5	684	22	AAH44248	Rice phytoene synt	
30	468	20.2	464	22	AAH44248	Physcomitrella pat	
31	458.5	20.2	1509	15	AAO64910	Thermus thermophil	
32	442	19.5	749	19	AAV03882	phytoene synthase	
33	420	18.5	766	21	AAZ28141	phytoene synthase	
34	378	16.7	56609	21	AAA81459	Rice phytoene synt	
35	378	16.7	349980	21	AAF21609	N. meningitidis pa	
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37	364	16.0	1198	12	AAO13718	phytoene synthase	
38	364	16.0	1198	17	AAT40791	phytoene synthase	
39	364	16.0	1198	17	AAT41743	phytoene synthase	
40	364	16.0	1198	17	AAT37093	E. herbicola phyto	
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43	359.5	15.8	945	25	ABD48802	Rhodococcus erythr	
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45	356.5	15.7	870	25	ABZ40269	N. gonorrhoeae nuc	

ALIGNMENTS

RESULT 1

AA166366

AA166366 standard; cDNA, 1728 BP.

AA166366;

29-JAN-2002 (first entry)

Nicotiana tabacum phytoene synthase coding sequence #1.

Phytoene synthase; zeta carotene desaturase; herbicide; transgenic plant; plant growth regulator; herbicidal; tobacco; ss.

Nicotiana tabacum.

Key

Location/Qualifiers

244..1566

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FT      /tag= a
FT      /product= "phytoene synthase"
XX      DE10022362-A1.
XX      15-NOV-2001.
XX      08-MAY-2000; 2000DE-1022362.
XX      08-MAY-2000; 2000DE-1022362.
XX      (FARB ) BAYER AG.
XX      Buech M, Hain R;
XX      MPI; 2002-027336/04.
XX      P-P8DB; AAM51841.
XX      New nucleic acid encoding tobacco zeta-carotene desaturase, useful for
XX      screening compounds with herbicidal activity -
XX      Claim 14; Page 12-17; 44pp; German.
XX      The present invention provides the protein and coding sequences of
XX      phytoene synthases and zeta-carotene desaturase from Nicotiana tabacum.
XX      The sequences can be used to identify compounds capable of altering the
XX      expression of these genes, which are therefore useful as plant growth
XX      regulators and herbicides. They can also be used to produce transgenic
XX      plants. The present sequence is the coding sequence of a tobacco
XX      phytoene synthase.
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Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:            24      Gaps:        0
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OY      41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgGlyLeuValSerGlyValArgGlnArgTrp 60
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DB      424 AATTTTGGCTCTTAAATTCCTGATCCAAATATTTATGCTTGGGTGATCAAGAACTGAA 483
OY      81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThr 100
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OY      361 ArgLysPhePheAspGluSerGluValValThrGluLeuAspSerAlaSerArgTrp 380
DB      1324 AGGAAATCTCTTATATGATGACAGAAAGGTGTCAACAACCTGCTGATGATGATGG 1383
OY      381 ProValLeuThrAlaLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAsp 400
DB      1384 CCTGTGTTAAACAGGCTGCTGTGTATCGCAAGATATTTGACGAGATTGAAGCCAACGAC 1443
OY      401 TyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuPro 420
DB      1444 TACAAACATTCACAGAGAGGCTTATATTTAGCAAGCCAAAGAACTTTCACCTTCCC 1503
OY      421 IleAlaTyrAlaLysSerLeuValProProAsnArgThrSerSerProLeuAlaLysThr 440
DB      1504 ATTGCTTATCAAAATATCTTTGTCGCCCTTAATGAACTTCTCTCCACAGAAAGACA 1563

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RESULT 2
 ABE13568 standard; DNA; 1573 BP.
 ID ABE13568;
 XX ABE13568;
 AC
 XX
 DT 12-JUN-2003 (first entry)
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 DE Tobacco phytoene synthase DNA.
 XX
 KW Zeaxanthin epoxidase; zeaxanthin; carotenoid; inhibitor;
 KW transgenic plant cell; alpha-tocopherol; food supplementation;
 KW tobacco; phytoene synthase; Fys; ds.
 XX
 OS Nicotiana tabacum.

XX WO2002103021-A2.
 XX 27-DEC-2002.
 XX 19-JUN-2002; 2002WO-BP06810.
 XX 19-JUN-2001; 2001EP-0114661.
 XX (VKAM/) VON KAMEKE K.
 XX Sandmann G, Roemer S, Luebeck J, Adomat C, Kauder F;
 XX WPI; 2003-167525/16.
 DR Increasing zeaxanthin and total carotenoid contents of plants, useful
 PT for food supplementation, by inhibiting activity of zeaxanthin
 PT epoxidase -
 PT
 PS Examples; Page 34-35; 52pp; German.
 XX
 CC This invention describes a novel method of increasing the zeaxanthin
 CC and/or total carotenoid contents in transgenic plant cells, plants or
 CC other host cells or organisms (e.g. algae) by inhibiting the endogenous
 CC zeaxanthin epoxidase (ZEP) activity. The invention also discloses
 CC transgenic plant cells or plants, their harvested products, replicative
 CC material (protoplasts, calli, seeds, tubers and cuttings) and
 CC descendants, produced by the novel method. The method is used to increase
 CC production of zeaxanthin and total carotenoids (including the therapeutic
 CC antioxidant alpha-tocopherol) for food supplementation. This sequence
 CC represents a polynucleotide corresponding to the tobacco (Nicotiana
 CC tabacum) phytylene synthase (Pys) gene which is used to describe the
 CC method of the invention.
 XX
 SQ Sequence 1573 BP; 475 A; 270 C; 390 G; 432 T; 6 other;

Alignment Scores:
 Pred. No.: 26-220 Length: 1573
 Score: 2143.50 Matches: 425
 Percent Similarity: 96.83% Conservative: 3
 Best Local Similarity: 96.15% Mismatches: 12
 Query Match: 94.43% Indels: 3
 DB: 25 Gaps: 1

US-09-847-081B-2 (1-440) x ABX13568 (1-1573)

QY 1 MetSerMetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerangly 20
 DB 10 ATGACCATGTCGTGCTTGTGTGGATTGTTTCCCAATTCGAGGTCCTCAATGGG 69
 QY 21 ThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerxPheLeu 40
 DB 70 AAGAGATTCCTGATTCAGTCGAGATGGAACCGGCTCTTGATCATCCAGGTTCTTA 129
 QY 41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgGlyLeuGlyGly---ArgGlnArg 59
 DB 130 GCTTCAGAGTGAATTTGATGTGGAATGGAGATCAAGAAAGCCGGAGAGCAAGAAAG 189
 QY 60 TrpAsnPheGlySerLeuLeuAlaAspProArgTrpSerCysLeuGlyGlySerArgThr 79
 DB 190 TGGAAATTTGGCTCTTAATTCAGATTCAAGATATGATGCTTGGNNNGATCAAGAACT 249
 QY 80 GluLysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMet 99
 DB 250 GANNNTGAGAGCACTTCTCTGTACAGTCACAGTTGGTGGCTAAGCCACCTGAGAAAGT 309
 QY 100 ThrValSerSerGlyLysValTyrAspValValLeuLeuGlnAlaAlaLeuValLys 119
 DB 310 ACTGTCTCATCAGAGAAAGAGGTATGTATGTGTGATTTAAAGCAGCAGCTTTAGTAAG 369
 QY 120 ArgGlnLeuArgSerThrAspAspLeuGluValLysProAspIleValValProGlyAsn 139
 DB 370 AGGCAAGCTGAGATCTAACGATGATTTAGAAAGGACCGGATATTGTTGTCACAGGAAT 429

QY 140 LeuGlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLys 159
 DB 430 TTGGGCTTGTTGATGGAAGCATATGATGCTTGGCCGAAGATGTGCAAGATGCAAG 489
 QY 160 ThrPheTyrLeuGlyThrLysLeuMetThrProGluValArgArgAlaIleTrpAlaIle 179
 DB 490 ACATTTCCTTAGGAAACCAAGCTATATGACCCAGAGAAAGAAAGAGCTATCTGGCAATA 549
 QY 180 TyrValTrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThr 199
 DB 550 TATGTGTGTGAGAGAACGATGAGCTGTGTGATGGCCCTTAATGATCCACATAACT 609
 QY 200 ProGlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPhe 219
 DB 610 CCGCAAGCTTTATAGATAGTGGGAGACCGAGCTGGAAGATTA-AACAGTGGCCGGCATTT 668
 QY 220 AspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnPro 239
 DB 669 GATATGCTTGATGCTGCTTATCCGATCTGTCCAGATTTCCTGTTGATATTCAGCCA 728
 QY 240 PheArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrIleThrPhe 259
 DB 729 TTCAGAGATATGATTTGAAGAGATGGATVGAACCTGTGGAATCCAGATACAAAACCTTTC 788
 QY 260 AspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValPro 279
 DB 789 GATAGCTATATCTCTATATGTTACTATGTGTGCTGATCTGATGATTAATGAGTTCCTCA 848
 QY 280 ValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeu 299
 DB 849 GTTATGGTATTTGACCTGATCAATCAAGCAACACAGAGAGTATATATGCTCTTTG 908
 QY 300 AlaLeuGlyLeuAlaAsnGluLeuThrAsnIleLeuArgAspValGlyLysAspAlaArg 319
 DB 909 ACTTTAGGCTTGCAATCACTAACCAATATCTCAGATGATGAGAAAGATGCCAGA 968
 QY 320 ArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlyLeuSerAspGluAsp 339
 DB 969 AGAGGAAGATATCTTCTCTCAGATATATTTAGACAGGAGGCTCTCCGACCAAGAC 1028
 QY 340 IlePheAlaGlyArgValThrAspLysTrpArgAsnPheMetLysGlnIleGlnArg 359
 DB 1029 ATATTGCTGGAAGAGTACATGATPAGTGAAGAACTTTATGAGAAACCAATTCAGAGG 1088
 QY 360 AlaArgLysPhePheAspGluSerGlyLysGlyValThrGluLeuAspSerAlaSerArg 379
 DB 1089 GCGAGGAATTCCTTGATGAGATCAAGAGAAAGGTGCACAGAACTGACTGCTGTGTAGA 1148
 QY 380 TrpProValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsn 399
 DB 1149 TGCCCTGTGTAAACGCCCTGCTGTGTATGCAAGATATTTGAGAGATTTGAAACCCAAC 1208
 QY 400 AspTyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeu 419
 DB 1209 GACTATCAACAACCTTCAAGAGAGGCTTATGTTAGCAAGCCAAAGAACTTCTCACCTTG 1268
 QY 420 ProIleAla-TyrAlaLysSerLeuValProProAsnArgThrSerSerProLeuAlaLys 439
 DB 1269 CCCATTGCTTTATGCAAAATCTTTGTGCCCCCTTAATGAAACTTCTCTCCACTAGCAAA 1328
 QY 439 sThr 440
 DB 1329 GACA 1332
 DB
 RESULT 3
 AA03880
 ID AA03880 standard; cDNA; 1826 BP.
 XX AA03880;
 AC
 XX
 DT 29-APR-1998 (first entry)
 XX

DE Phytoene synthase coding sequence from N. tabacum.
 XX Phytoene synthase; transgenic plant; enhanced carotenoid synthesis;
 KW ultra violet absorber; food colour; ss.
 XX Nicotiana tabacum.
 OS
 FH Key Location/Qualifiers
 FT CDS 367..1599
 FT /*tag= a
 XX
 EN US5705624-A.
 XX
 PD 06-JAN-1998.
 XX
 PF 27-DEC-1995; 95US-0579667.
 XX
 PR 27-DEC-1995; 95US-0579667.
 XX
 PA (DELL/) DELLA-CIOPPA G. R.
 PA (FITZ/) FITZMAURICE W. P.
 PA (GRILL/) GRILL L. K.
 PA (HELL/) HELLMANN G. M.
 PA (KUMAGI/) KUMAGAI M. H.
 PI Della-Cioppa GR, Fitzmaurice WP, Grill LK, Hellmann GM,
 PI Kumagai MH;
 XX
 XX WPI; 1998-086196/08.
 DR P-PSDB; AAM41059.
 XX
 XX DNA encoding tobacco phytoene synthase polypeptides - useful for
 PT producing recombinant polypeptides or transgenic plants
 XX
 ES Claim 1: Column 27-30; 25pp; English.
 XX
 XX This sequence encodes the phytoene synthetase from Nicotiana tabacum.
 CC The phytoene synthetase coding sequence represents a cDNA of the
 CC invention. The isolated nucleic acid molecules are used for producing
 CC recombinant polypeptides or transgenic plants with enhanced ability to
 CC synthesize carotenoids. Phytoene has been used as a ultra violet absorber
 CC and other carotenoids have been used as food colours, animal feeds and in
 CC the pharmaceutical and cosmetics industries.
 CC
 XX
 SQ Sequence 1826 BP; 589 A; 282 C; 433 G; 522 T; 0 other;
 Alignment Scores:
 Pred. No.: 3,61e-186 Length: 1826
 Score: 1826.00 Matches: 362
 Percent Similarity: 88.61% Conservative: 27
 Best Local Similarity: 82.46% Mismatches: 21
 Query Match: 80.44% Indels: 29
 DB: 19 Gaps: 4
 US-09-847-081B-2 (1-440) x AAV03880 (1-1826)
 QY 3 MetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGlyThrGly 22
 Db 367 ATGTCTGTGCTTGTATAGGCTGTTCACCT--TGTGAGGTCTCAAAATGGGACAGGA 423
 QY 23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42
 Db 424 TTCTTGGATTCACTAAGGAGGAGAAACCGGTTTGTGACTCGTCG-----AGG 471
 QY 43 AspArgAsnLeuMetTrpAsnGlyValArgIleValArgGlyValArgGlyValArgTrpAsn 62
 Db 472 CATGGAATTGATGTCGCAATGAGAGATCAAAACAGCGTGCAGCAACAAAGGTGGAATTT 531
 QY 63 GlySerLeuIleAlaAspProArgTrpSerCysLeuGlyGlySerArgThrGluLeuGly 82
 Db 532 GGT----- 534
 QY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMet---ThrVal 101

Db 535 -----TCTGACGCTCGCATGTGCTACACCAACGGAGAAATGCGACAAATG 585
 QY 102 SerSerGluValSerValTyrAspValValLeuValGlnAlaLeuValLysArgGln 121
 Db 586 ACATCAGACAGAAAGTTATGATGTGTATGAAACAGACGCTTATGTAAGAAAGCG 645
 QY 122 LeuArgSerThrAspAspLeuGluValLysProAspIleValValProGlyAsnLeuGly 141
 Db 646 CTGAGATCTACTGATGATTTAGAAAGTGAACCGGAGATCCCTCCCGGGAATTTGAGC 705
 QY 142 LeuLeuSerGluValTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPhe 161
 Db 706 TTGTTAAGTAGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 765
 QY 162 TyrLeuGlyThrLysLeuMetThrProGluLysArgArgAlaIleTyrPheVal 181
 Db 766 TACTTAGAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 825
 QY 182 TrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGln 201
 Db 826 TGGTGACAGAGAACAGATGAACTTTGATGGCCGGAATCATATATATATATATATATAT 885
 QY 202 AlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyValArgProPheAspMet 221
 Db 886 GCCTTAGATAGTGGGAGAACCGCGCTGGAAGATGTTTCAGTGGCGGCAATTTGATATG 945
 QY 222 LeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArg 241
 Db 946 CTCGATCTCTCTTTGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1005
 QY 242 AspMetIleGluGlyMetCysMetAspLeuTrpLysSerArgTrpLysThrPheAspGlu 261
 Db 1006 GATATGATTAAGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1065
 QY 262 LeuTyrLeuTyrCysTrpValAlaGlyThrValGlyLeuMetSerValProValMet 281
 Db 1066 CTATACCTATATGTTATGTTACGTTGCTGTGATGCTGTGATGATGATGATGATGATGAT 1125
 QY 282 GlyIleLeuAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeu 301
 Db 1126 GGTATGTCACCTGATTTAAAGGCAACAGAGGTATATATATATATATATATATATAT 1185
 QY 302 GlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGly 321
 Db 1186 GGAATCCCAATCAACTAACCAATCTCAGAGATTCGAGAGATGCGAAGAGAGAGGA 1245
 QY 322 ArgValTyrLeuProGluAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePhe 341
 Db 1246 AGAGTCTACTTAACTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1305
 QY 342 AlaGlyArgValThrAspLysTrpArgAsnPheMetLysValGlnIleGlnArgAlaArg 361
 Db 1306 GCTGGAAGAGTGAATGATTAATAGAGAGCTTTATGAGAGAGAGAGAGAGAGAGAG 1365
 QY 362 LysPhePheAspGluSerGluValValThrGluLeuAspSerAlaSerArgTrpPro 381
 Db 1366 AAATTTCTTCAACAG 1425
 QY 382 ValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGlnAlaAsnAspTyr 401
 Db 1426 GTATGGGACATCTTGTGTTGATCCGCGCAGATCTCAGACAGATGTAAGCAATGACTAC 1485
 QY 402 AsnAsnPheThrArgAlaGlyValValSerLysProLysLysLeuThrLeuProIle 421
 Db 1486 AACCACTTCCAG 1545
 QY 422 AlaTyrAlaLysSerLeuValProProAsnArgThr-SerSerProLeuAlaLys 439
 Db 1546 GCTTATGCAAAATCTTGTGCCCCCTTACAGAACTCTTGTACCTTACCTAAG 1600
 RESULT 4
 AAI66367

RESULT 5
AAV03881
ID AAV03881 standard; cDNA; 1814 BP.
XX
XX AAV03881;
XX
XX 29-APR-1998 (first entry)
XX
XX Phytoene synthase coding sequence from N. tabacum.
DE Phytoene synthase coding sequence from N. tabacum.
XX
XX Phytoene synthase; transgenic plant; enhanced carotenoid synthesis;
KM ultra violet absorber; food colour; ss.
XX
XX Nicotiana tabacum.
XX
XX
FH Key Location/Qualifiers
FT CDS 363..1595
ET /*tag= a
XX
XX US5705624-A.
XX
XX 06-JAN-1998.
PD
XX
XX 27-DEC-1995; 95US-0579667.
PF
XX
XX 27-DEC-1995; 95US-0579667.
PR
XX
XX (DELL/) DELLA-CIOPPA G R.
PA (FITZ/) FITZMAURICE W P.
PA (GRIL/) GRILL L K.
PA (HELL/) HELLMANN G M.
PA (KUMA/) KUMAGAI M H.
PI Della-Cioppa GR, Fitzmaurice WP, Grill LK, Hellmann GM,
PI Kumagai M;
XX
XX WP1; 1998-086196/08.
DR P-PSDB; AAM41060.
XX
XX
XX DNA encoding tobacco phytoene synthase polypeptides - useful for
PT producing recombinant polypeptides or transgenic plants
XX
XX
XX Claim 1; Column 33-36; 25pp; English.
XX
XX
XX This sequence encodes the phytoene synthetase from Nicotiana tabacum.
CC The phytoene synthetase coding sequence represents a cDNA of the
CC invention. The isolated nucleic acid molecules are used for producing
CC recombinant polypeptides or transgenic plants with enhanced ability to
CC synthesise carotenoids. Phytoene has been used as a ultra violet absorber
CC and other carotenoids have been used as food colours, animal feeds and in
CC the pharmaceutical and cosmetics industries.
XX
XX
SQ Sequence 1814 BP; 577 A; 281 C; 441 G; 515 T; 0 other;

Alignment Scores:
Pred. No.: 2,886-183 Length: 1814
Score: 1799.00 Matches: 356
Percent Similarity: 87.93% Conservative: 30
Best Local Similarity: 81.09% Mismatches: 24
Query Match: 79.25% Indels: 29
DB: 19 Gaps: 4

US-09-847-081B-2 (1-440) x AAV03881 (1-1814)

OY 3 MetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGlyThrGly 22
DB 363 ATGCTCTGTCCTTGTATGCGTTTTCACCT--TGTGAAGTCTCAATGGGACAGGA 419
OY 23 LeuLeuAspSerValAlaGluGlyValAsnArgValPheValSerSerArgPheLeuAlaArg 42
DB 420 TTCCTTGATTCAGTCCGGAGGGAACCGGGTTTTCGATTCGTCG-----AGG 467
OY 43 AspArgAsnLeuMetTrpAsnGlyArgGlyLeuGlyGlyArgGlnArgTrpAsnDhe 62

DB 468 CATAGCAATTTAGTGTCAATGAGAGAAACAGAGAGGTGTGAACAAAGTGCATTTT 527
OY 63 GlySerLeuLeuAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluLeuGly 82
DB 528 GGT----- 530
OY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGlyMet---ThrVal 101
DB 531 -----TCTGTAAGTCTGCTATGTGTGCTTACACCGCGGAGAAATGGCAGCATG 581
OY 102 SerSerGluLeuValValTyrAspValValLeuLeuGlnAlaAlaLeuValValArgGln 121
DB 582 ACATCAGACAGACAGATGTTTATGATGTGTTTAAACACACAGCTTTAGTGAAGACGAG 641
OY 122 LeuArgSerThrAspAspLeuGluValValPheAspValValProGlyAsnLeuGly 141
DB 642 TTGAGATCTGCTGATGATTTTGAAGTGAAGCCGAGATCCCTCTCCCGGAAATTTAGC 701
OY 142 LeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGlyTyrAlaLeuThrPhe 161
DB 702 TTGTTGAGTGAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 761
OY 162 TyrLeuGlyThrLeuLeuMetThrProGluArgArgAlaLeuTrpAlaLeuTyrVal 181
DB 762 TACTTAGGAACCAAGCTTAATGACTCCAGAGAGAAAGGCGCTATTGGCGCAATATATGTG 821
OY 182 TrpCysArgArgThrAspArgLeuValAspGlyProAsnAlaSerHisileThrProGln 201
DB 822 TGGTCAGAGAAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 881
OY 202 AlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMet 221
DB 882 GCCTTATATAGTGTGGAGAACCGGCTTGAAGATGTTTTCAGCGGCGCATTTGATATG 941
OY 222 LeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArg 241
DB 942 CTCGATGCTGTTTGTCCGATGACTGTTCCAGCTTCAGTTGATATTCAGCCCTTCAGA 1001
OY 242 AspMetIleGluGlyMetArgMetAspLeuTrpPheSerArgTyrLeuThrPheAspGly 261
DB 1002 GATATGATGAGAGAAAGCGATGACTTGAAGAGTGAAGATATGAAGAACTTTGATGAG 1061
OY 262 LeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMet 281
DB 1062 CTTTACTCTATTTCTTATTAAGTTGCTGCTGATCGTTGGTTGATGATGATTTCCAAATATG 1121
OY 282 GlyIleAlaProGluSerLeuValAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeu 301
DB 1122 GGTATTCACCTGATTCMAAGGCAACAGAGAGCTATATATATGACGCTTTGGCTTTA 1181
OY 302 GlyLeuAlaAsnGluLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgGly 321
DB 1182 GGAATCGGAATCACTACAGAACATACTCAGGAGATGTGGAGAAAGTCCAGAGAGGA 1241
OY 322 ArgValTyrLeuProGluAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePhe 341
DB 1242 AGAGTCTACTTACTCTCAAGATGAATGACAGGCAAGTCTCTTCAGCATGACATATTT 1301
OY 342 AlaGlyArgValThrAspLeuTrpAsnAsnPheMetLeuLeuGlnIleGlnAlaArgAlaArg 361
DB 1302 GCTGGAAGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1361
OY 362 LysPhePheAspGluSerGluValValThrGluLeuAspSerAlaSerArgTrpPro 381
DB 1362 AAGTCTTTCATGAGGAGAGAGAGGAGTTCACAACTGAGCTGATGAGATGAGTCCCT 1421
OY 382 ValLeuThrAlaLeuLeuLeuTyrArgGlyIleLeuAspGluIleGlnAlaAsnAspTyr 401
DB 1422 GTATGGGACATCTTGTCTGTGTACCGCAATCTGACAGAGATGAGCAAGATGATAC 1481
OY 402 AsnAsnPheThrArgArgAlaTyrValSerLeuProLeuLeuLeuLeuLeuLeuLeu 421

QY 380 TTPProValLeuThrAlaLeuLeuLeuTyArgLysIleLeuAspGluIleGluAlaAsn 399
 Db 1415 TGGCTGTATGGGCTTCTTGTGTACCGCCAGATACTGACGAGTCGAAGCCAAAT 1474
 QY 400 AAPTYYAaenPheThrArgArgAlaTyValSerLysProLysLysLeuLeuThrLeu 419
 Db 1475 GACTACAAACAACTTACAAAGAGAGCTTATGAGCAAAATCAAAAGACTTAATTCCTTA 1534
 QY 420 ProIleAlaTyArgLysSerLeuValProPheAsnArgThr-SerSerProLeuAlaTy 439
 Db 1535 CCTATTGCTATGCAAAATCTCTTGTGCCCCCAAGAACTCTTCTCTTACTTA 1594
 QY 439 s 439
 Db 1595 G 1595
 Db 1595 G 1595
 RESULT 7
 AAV03879
 ID AAV03879 standard; cDNA; 1316 BP.
 AC AAV03879;
 XX
 DT 29-APR-1998 (first entry)
 XX
 DE Phytoene synthase coding sequence from N. benthamiana.
 XX
 KM Phytoene synthase; transgenic plant; enhanced carotenoid synthesis;
 XX ultra violet absorber; food colour; ss.
 OS Nicotiana benthamiana.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1242
 FT /*tag= a
 XX
 XX US5705624-A.
 XX
 PD 06-JAN-1998.
 XX
 PE 27-DEC-1995; 95US-0579667.
 XX
 PR 27-DEC-1995; 95US-0579667.
 XX
 PA (DBL/) DELLA-CIOPA G. R.
 PA (FITZ/) FITZMAURICE W. P.
 PA (GRILL/) GRILL L. K.
 PA (HELL/) HELLMANN G. M.
 PA (KOMA/) KOMAGAI M. H.
 XX
 PI Della-Ciopa GR, Fitzmaurice WP, Grill LK, Hellmann GM;
 PI Kumagai MH;
 XX
 DR WPI; 1998-086196/08.
 DR P-PSDB; AAW41058.
 XX
 PT DNA encoding tobacco phytoene synthase polypeptides - useful for
 PT producing recombinant polypeptides or transgenic plants
 XX
 PS Claim 1; Column 21-26; 25pp; English.
 XX
 XX This sequence encodes the phytoene synthetase from Nicotiana benthamiana.
 CC The phytoene synthetase coding sequence represents a cDNA of the
 CC invention. The isolated nucleic acid molecules are used for producing
 CC recombinant polypeptides or transgenic plants with enhanced ability to
 CC synthesise carotenoids. Phytoene has been used as a ultra violet absorber
 CC and other carotenoids have been used as food colours, animal feeds and in
 CC the pharmaceutical and cosmetics industries.
 XX
 SQ Sequence 1316 BP; 403 A; 221 C; 342 G; 350 T; 0 other;
 Alignment Scores: 1.73e-179 Length: 1316
 Pred. No.: 1762.00 Matches: 347
 Score:

Percent Similarity: 87.04% Conservative: 29
 Best Local Similarity: 80.32% Mismatches: 28
 Query Match: 77.62% Indels: 28
 DB: 19 Gaps: 4
 US-09-847-081b-2 (1-440) x AAV03879 (1-1316)
 QY 3 MetSerValAlaLeuLeuThrPValValSerProThrSerGluValSerAsnGlyThrGly 22
 Db 1 ATGCTCTTGCCTTGTATGGGTTGTTCACT---TGTAAGGCTCAAAATGGACAGGA 57
 QY 23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerArgPheLeuAlaArg 42
 Db 58 TTCTTGATTCAAATCCGGAGAGGAAACCGGCTTTTATTTGATTCGTCG-----AGG 105
 QY 43 AspArgAsnLeuMetTPaenGlyArgGlyLeuGlyGlyGlyArgGlnArgGlnArgPhe 62
 Db 106 CATAGCAATTTAGTGTCAAATGAGAGAAACAGAGAGTGTGCAACAAATGTGGAATTT 165
 QY 63 GlySerLeuIleAlaAspProArgTySerCysLeuGlyGlySerArgThrGluGly 82
 Db 166 GGT----- 168
 QY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGlyMet---ThrVal 101
 Db 169 -----TCTGTAAGCTCTGCTATGTGGCTACACCGCGGAGAAATGGCGACGATG 219
 QY 102 SerSerGluLysValTyArgPValValLeuGlyGlnAlaAlaLeuValLysArgGln 121
 Db 220 ACATCAGACAGAGTGTTATGATGTGTATGAAACAAACAGCTTATGTGAAAGGCGAG 279
 QY 122 LeuArgSerThrAspAspLeuGluValLysProAspIleValValProGlyAsnLeuGly 141
 Db 280 TTGAGATCTACTATGATTTAGAAAGTGAAGCGGAGATCCCTCCCGGGGAATTTGAGC 339
 QY 142 LeuLeuSerGluAlaTyArgAspArgCysGlyGluValCysAlaGlyTyAlaLysThrPhe 161
 Db 340 TTGTTGAGTGAAGCATGTAGTATAGGTGAGCAAGTATGTGCAGATGTGGAAGACATTT 399
 QY 162 TyrlenuGlyThrLysLeuMetThrProGluArgArgArgAlaIleTPaAlaIleTyVal 181
 Db 400 TACTTAGAACTATGCTTAATGACTCCAGAGAGAAAGGGCTATTGGGCAATATATGTA 459
 QY 182 TrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGln 201
 Db 460 TGGTGCAGAGAACAGACGAACTTGTGATGCCCCGAAATGATCATATTAATCCACAA 519
 QY 202 AlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMet 221
 Db 520 GCCTTAGATAGTGGGAAGACCGGCTGGAAGATGTTTCAATGGGCGGCATTTGACATG 579
 QY 222 LeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArg 241
 Db 580 CTCGATCTGCTTGTTCGATACGTTTCAGTTTCCAGTTGATATGACCGCTTGAGA 639
 QY 242 AspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyTrpLysThrPheAspGlu 261
 Db 640 GATATGATCGAAGAAAGCGTATGCACTTGAGAAAGTCGAGATACAAAACTTTGAGAG 699
 QY 262 LeuTyrlenuTyrcysTyTyValAlaGlyThrValGlyLeuMetSerValProValMet 281
 Db 700 CTATACCTAATATGTTATATGCTGTGCTGATAGTTGGTGTGATGATGTTCCAAATATG 759
 QY 282 GlyIleAlaProGluSerLysAlaThrThrGluSerValTyArgAlaAlaLeuAlaLeu 301
 Db 760 GGCATTCGACCTGATATAAGGCAACAGAGAGTATATATATGAGCTTTGGCTTTG 819
 QY 302 GlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGly 321
 Db 820 GGTATCGCAATCACTACCAATCTCTCAGAGATTCGAGAGAAATGCCAAGAGAGGA 879
 QY 322 ArgValTyrlenuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePhe 341

Db 880 AGAGTCTACTTACCTCAGATGAATTAGCAGACGCGTCTCTCCGACGATGACATATT 939
 QY 342 AlAGlYArGValThrAspLySTrpArgAnpMethLysLysGlnIleGlnArgAlaArg 361
 Db 940 ACTGGAAAAGTACATGATTAATGAGAACACTTATGTAACAAACATTCAGAGGGCAGA 999
 QY 362 LysPhepAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrpPro 381
 Db 1000 AAGTCTTCAATGAGGACAGAGAGAGATTACAACTAGCTCAGCTGACGATGAGCT 1059
 QY 382 ValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGlnIleGlnAlaAsnAspTyr 401
 Db 1060 GATATGGACATCTTGTCTGTGTAACGCCAAATACCGACAGATCGAACCCATGACTAC 1119
 QY 402 AsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuProIle 421
 Db 1120 AACAACTTACAAAGAGACTTATGTGACCAATCAAAAGACGTAATTTCTTACTATT 1179
 QY 422 AlaTyrAlaLysSerLeuValProProAsnArgThr 433
 Db 1180 GCTTATGCAAAATCTCTGTGCCCCCTACAGAACT 1215

RESULT 8

AAQ9323 standard; cDNA; 1591 BP.

AAQ9323;

13-APR-1996 (first entry)

Melon phytoene-synthase gene.

melon; phytoene-synthase; ripening; cDNA library; fruit; ME15;
 tomato; TOM5; probe; hybridisation; polymerase chain reaction; PCR;
 antisense; transgenic plant; crop improvement; carotenoid; vector;
 88.

Cucumis melo.

MO9602650-A2.

01-FEB-1996.

06-JUL-1995; 95WC-GB01603.

22-SEP-1994; 94GB-0019081.

18-JUL-1994; 94GB-0014505.

(ZENEC) ZENECA LTD.

Grierson D, John I, Karvouni Z, Taylor J, Turner A,

Watson C;

WPI, 1996-105912/11.

New isolated DNA encoding melon phytoene synthase - used to
 transform plants to modify carotenoid content and related
 characteristics in plant parts, partic. fruit

Claim 2; Page 15-16; 22pp; English.

The sequence encodes melon phytoene-synthase (ME15 gene), and is
 almost full-length. The sequence has been isolated as a cDNA clone
 from a ripening-related cDNA library derived from climacteric melon
 fruit, using the tomato phytoene-synthase cDNA (TOM5) as a
 heterologous probe. The ME15 gene 5'-end has also been isolated by
 polymerase chain reaction and sequenced. The DNA may be used in
 sense or antisense constructs to modify gene expression in plants.
 The carotenoid content and related characteristics of plant parts
 (particularly fruit) may be modified in this way.

Sequence 1591 BP; 507 A; 237 C; 395 G; 452 T; 0 other;

Alignment Scores:

Pred. No.: 3,486-178 Length: 1591
 Score: 1751.00 Matches: 344
 Percent Similarity: 86.67% Conservative: 33
 Best Local Similarity: 79.08% Mismatches: 34
 Query Match: 77.14% Indels: 24
 DB: 17 Gaps: 3

US-09-847-081B-2 (1-440) x AAQ9323 (1-1591)

QY 1 MetSerMetSerValAlaLeuLeuTyrValValSerProThrSerGluValSerAnGly 20
 Db 258 CTCAAAATGTCGTGTCCTGTATGAGGTGTTCTCTCT--TGTGAGTCTCAATGAGG 314
 QY 21 ThrGluLeuLeuAspSerValArgGluLysAnGlyValPheValSerSerArgPheLeu 40
 Db 315 ACAAGTTTACAGAAATCAGTCGCGAGGAGAAACGTTTTTTTGATTCAATCG----- 365
 QY 41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgIleLysLysGlyValArgGlnArgTrp 60
 Db 366 ---AGCATAGGAATTTGTGTGTCATAGAGAAATCAATAGAGT----- 407
 QY 61 AsnPheGlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGlu 80
 Db 408 -----GGTGAAGAACCAACTAAT 425
 QY 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThr 100
 Db 426 AATGACGGAATTTTGTGACGCTGCTGATTTTGGTACTCCATCTGGAAGAACGAGCG 485
 QY 101 ValSerSerGluLysLysValTyrAspValValLeuLysGlnAlaAlaLeuValLysArg 120
 Db 486 ATGACATCGAAGACAGATGCTCATGATGTGTTTGAAGCAGCGACCTGTGTGAAGAG 545
 QY 121 GlnLeuArgSerThrAspAspLeuGluValLysProAspIleValValProGlyAsnLeu 140
 Db 546 CAACTGAGATCTACCAATAGATGATGAGAGTGAAGCGGATATACCTAATCCGGGGAATTGG 605
 QY 141 GlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThr 160
 Db 606 GCGTTGTGAGGAAAGCATATGATAGTGTGTGTAAGTATGACAGATATGCAAGAGCG 665
 QY 161 PheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTyrAlaIleTyr 180
 Db 666 TTTAACTTAGAACAATCTATGCTAATGACTCCCGAGAGAAAGGCTATCTGGCAATATAT 725
 QY 181 ValTyrCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrPro 200
 Db 726 GTATGTCAGAGAAACAGATGAATGACTTGTGATGGCCCAACGATCATATATTAACCCG 785
 QY 201 GlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAsp 220
 Db 786 GCAGCCTTAGATAGGTGGGAAATAGGCTAGAAAGTGTTCATAGGGCGGCAATTTGAC 845
 QY 221 MetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPhe 240
 Db 846 ATGCTCGATGCGCTTGTTCGATACAGTTTCTAATTTCCAGTTGATATTAACGCAATTC 905
 QY 241 ArgAspMetIleGluGlyMetArgMetAspLeuTyrLysSerArgTyrLysThrPheAsp 260
 Db 906 AGAGATATGATTAAGAGAAATGCGTATGCACTTGAGAAATGAGATACAAAACCTTCAC 965
 QY 261 GluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProVal 280
 Db 966 GAACATATACCTTTATGTTATATGCTTCGTATCGGTGGGTGATGATAGTTCATCAAT 1025
 QY 281 MetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAla 300
 Db 1026 ATGGATATCGCCCTCGAATCAAGGCAACACAGAGCCGATATATATGCTGCTTGGCT 1085
 QY 301 LeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArg 320
 Db 1086 CTGGGGATCGCAATCATTAATCACTACATCTCAGAGATGTTGGAGAGATGCCGAGAGA 1145

QY 321 GlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle 340
 Db 1146 GGAAGAGCTACTTCTCCATGATGATATAGACAGCGAGCTATCGATGAGATATA 1205
 QY 341 PheAlaGlyArgValThrAspLysTrpArgAspMetLysGlnIleGlnArgAla 360
 Db 1206 TTTGCTGAGAGGCTACCGATTAATGAGAAATCTTTATGAAAGAAACAAATCATGTGGGCA 1265
 QY 361 ArgLysPhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrp 380
 Db 1266 AGAAAGTCTTTCATGAGAGCGAGAAAGCGTGACAGAAATGAGCTCAGCTATGATGATTC 1325
 QY 381 ProValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAsp 400
 Db 1326 CCGTATGGGCACTTTGGTCTTGTAACGCAAAATCACTAGATGAAAGCCATGAC 1385
 QY 401 TyrAsnAspMetThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuPro 420
 Db 1386 TACAACAACCTTCACAAAGAGACATATGTGAGCAATCAAGAAAGTTGATTCATTACTT 1445
 QY 421 IleAlaTyrAlaLysSerLeuValProAsnArgThrSerSer 435
 Db 1446 ATTCATATGCAAAATCTTGTGCTCTCTACAAAACCTGCTCT 1490

RESULT 9

AAV17247

ID AAV17247 standard; DNA; 1239 BP.

AC AAV17247;

DT 28-MAY-1998 (first entry)

DE MTOM5, modified phycoene synthase gene.

KW MTOM5; phycoene synthase; chloroplast targeting sequence; enzyme; tomato;
 protein expression enhancement; transgenic plant; carotenoid synthesis;
 lycopene; ds.

OS Lycopersicon esculentum.

FH Key Location/Qualifiers

FT CDS 1..1239

FT /tag= a

FT /note= "contains an intron"

FT exon 1..960

FT /number= 1

FT intron 961..990

FT /tag= c

FT /number= 1

FT exon 991..1236

FT /tag= d

FT MO9746690-A1.

PD 11-DEC-1997.

PF 23-MAY-1997; 97WO-GB01414.

PR 07-JUN-1996; 96GB-0011981.

PA (ZENNE) ZENNECA LTD.

PI Bird CR, Drake CR, Schuch MW;

DR WPI; 1998-042198/04.

PT P-PSDB; AAW41374.

XX Enhancing gene expression without or with reduced co-suppression -
 PT using altered DNA producing different RNA but same protein as
 PT natural gene, useful especially in plants to allow overexpression of
 PT a protein

XX Claim 9; Page 15-16; 32pp; English.
 PS This sequence represents the modified phycoene synthase gene MTOM5, which

CC is also a chloroplast targeting sequence. This sequence is used in the
 CC method of the invention for enhancing expression of a protein by an
 CC organism, comprising inserting into its genome a nucleotide sequence
 CC which produces different RNA on transcription to that of the gene already
 CC present, but produces the same protein on translation. Transgenic plants
 CC with enhanced ability to express a selected can be produced by the
 CC method. For example, the method can be used to achieve overexpression of
 CC a gene specifying an enzyme necessary for carotenoid synthesis in plants
 CC (especially phycoene synthase), to enhance carotenoid expression,
 CC e.g. overexpression of the carotenoid lycopene responsible for the red
 CC colouration of developing tomato fruit. Protein expression is enhanced by
 CC inserting a gene construct which is altered by maximising the
 CC dissimilarity of nucleotide usage whilst maintaining identity of the
 CC encoded protein. Known methods of increasing protein production by gene
 CC insertion sometimes result in low or no expression (co-suppression),
 CC especially when the recombinant and endogenous gene sequences are
 CC similar. The method allows enhanced expression whilst avoiding or
 CC reducing co-suppression, since sequence similarity between the two genes
 CC is sufficiently reduced.

SQ Sequence 1239 BP; 343 A; 247 C; 320 G; 329 T; 0 other;

Alignment Scores:

Pred. No.:	137e-177	Length:	1239
Score:	1744.00	Matches:	343
Percent Similarity:	86.61%	Conservative:	32
Best Local Similarity:	79.21%	Mismatches:	34
Query Match:	76.83%	Indels:	24
DB:	19	Gaps:	3

US-09-847-081B-2 (1-440) x AAV17247 (1-1239)

QY 3 MetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGlyThrGly 22
 Db 1 ATGAGCGTGGCACTTCTGGTGTGTGAGCCCA---TGCATGTGATTAACGGCACTTCA 57
 QY 23 LeuLeuAspSerValAlaGluGluValAsnArgValPheValSerSerArgPheLeuAlaArg 42
 Db 58 TTTATGAGAGGTGTGAGAGAGGTAAATGATTTCTTCAACAGTTCT-----CGT 105
 QY 43 AspArgAsnLeuMetTPAsnGlyArgIleLysGlyGlyArgGlnArgTrpAsnPhe 62
 Db 106 CACCTTAACCTTGTATTAACGAACGTTAAACGGGGA----- 144
 QY 63 GlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluLysGly 82
 Db 145 -----CGAGGTAAACAGCAACACGCT 168
 QY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSer 102
 Db 169 AGAAAGTCTTCAGTTAGATCAGCAATCTTGCAACACCTGCGGTGAGAACTATACT 228
 QY 103 SerGluLysLysValTyrAspValValLeuLysGlnAlaIleAlaLeuValLysArgGlnLeu 122
 Db 229 AGCAGCAAAATGTGTGACAGCTGTGCTTCTGTAACCTGCACTAGTTAAACGTCAAGTTA 288
 QY 123 ArgSerThrAspAspLeuGluValLysProAspIleValValProGluAsnLeuGlyLeu 142
 Db 289 CGTATGACTTAACGAACCTTAGAGTTAAACGTGACATTCATCTGAAACCTTGACCTT 348
 QY 143 LeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysTrpPheTyr 162
 Db 349 CTTTCTAGGCTTACGACATGCGAGAGGTTTGGCCAGAAATACGCTTAAACCTTCAAT 408
 QY 163 LeuGlyThrLysLeuMetThrProGluArgArgAlaIleTTPAlaIleTyrValTyr 182
 Db 409 TTGGGTACCAATGTGATGACCCGAAAGCGTGTGTCAATATGCGCTATTTAGCTTTGG 468
 QY 183 CysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAla 202

[illegible]

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FT XX /transl_except= (pos: 1057..1059, aa: Arg)
EN XX
PD XX MO200009722-A2.
PD XX 24-FEB-2000.
PF XX
PF XX 10-AUG-1999; 99MO-US18066.
XX XX
XX XX 10-AUG-1998; 98US-0096111.
PR XX 07-JUN-1999; 99US-0137977.
XX XX
XX XX (MONS ) MONSANTO CO.
XX XX
PI XX Brown SM, Elich TD, Heck GR, Kishore GM, Loguech EW, Loguech SJ;
PI XX Piller KJ, Rao S, Ream JE;
DR XX WPI; 2000-224351/19.
DR XX P-PSDB; AAY84101.
XX XX
XX XX Obtaining transgenic plant useful for controlling seed germination and
PT XX seedling growth comprises transgene comprising a sequence expressing
PT XX altered levels of an essential hormone
XX XX
XX XX Claim 45; Page 254-255; 267bp; English.
XX XX
XX XX The present sequence encodes a phytoene synthase polypeptide, which
CC XX is used in the method of the invention. The specification describes
CC XX methods for the inhibition and control of gibberellin acid levels.
CC XX Gibberellin acid levels may be inhibited or controlled by use of
CC XX a chimeric expression construct expressing a RNA or protein which
CC XX suppresses the gibberellin biosynthetic pathway sequence, diverts
CC XX substrate from the pathway, or degrades pathway substrates or products.
CC XX The methods uses copataly diphosphate synthase, 3beta-hydroxylase,
CC XX 2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta,3beta-hydroxylase
CC XX polynucleotides to achieve this. The method is used to control seed
CC XX germination and seedling growth especially to regulate gene products of
CC XX gibberellin biosynthetic pathway and restoration of normal seed
CC XX germination, in transgenic plants. The plants produced are gibberellin
CC XX deficient, and have shortened hypocotyl and/or epicotyl phenotypes
CC XX compared to normal plants.
XX XX
SQ XX Sequence 1239 BP; 376 A; 208 C; 316 G; 339 T; 0 other;
XX XX
XX XX Alignment Scores:
XX XX Pred. No.: 7,76e-177 Length: 1239
XX XX Score: 1737.00 Matches: 342
XX XX Percent Similarity: 86.37% Conservative: 32
XX XX Best Local Similarity: 78.98% Mismatches: 35
XX XX Query Match: 76.52% Indels: 24
XX XX DB: 21 Gaps: 3
XX XX
US-09-847-081B-2 (1-440) x AA299482 (1-1239)
XX XX
OY 3 MetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGlyThrGly 22
Db 1 ATGTCTGTTGGCTTGTATTATGGTGTGTTCTCT--TGTCAGCTCTCAAAATGGACAGT 57
OY 23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42
Db 58 TTCATGGAATCAGTCCGGAGGAGGAAACCGTTTTTTGATTATCG-----AGG 105
OY 43 AspArgAsnLeuMetTrpAsnGlyArgIleuSlyGlyGlyArgGlnArgTrpAsnPhe 62
Db 106 CARGAATTTTGCTGTCACATAGAGCAATCAATAGGT----- 144
OY 63 GlySerLeuIleAlaAspProArgTrgTrSerCysLeuGlyGlySerArgTrgGluGly 82
Db 145 -----GGTGAAGAAAGCAAACTAATATGCA 168
OY 83 SerThrPheSerValGlnSerSerLeuValAspProAlaGlyGluMetThrValSer 102
Db 169 CGGAATTTTCTGTAGGCTGTGCTATTTTGGCTACTCATCTTGAGAAACGACGATATCA 228

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Oy	103	SerGluYsLysValTyrAspValValLeuYsGlnAlaLeuValLysArgLysLeu	122
Db	229	TCGGAACGATGGCTATGATGATGGCTTTGAGCGAGCGCTTGTAAGAGGCACTG	288
Oy	123	ArgSerThrAspAspLeuGlnValLysProAspLleValProGlyAsnLeuGlyLeu	142
Db	289	AGATCTACCAATGAGTTAGTAAGTGAAGCCGATATACCAATTCGGGGGAAATTGGGCTTG	348
Oy	143	LeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyr	162
Db	349	TTGATGTGAAGCATATGATAGGTGGTGTGAAGTATGTGACAGATATGCAAAAGCGTTTAAAC	408
Oy	163	LeuGlyThrLysLeuMetThrProGluArgGlyAlaIleThrAlaIleTyrValTrp	182
Db	409	TTAGGAACCTATAGCTATGACTCCGACAGAGAAAGGCGTATCTGGGCATATATGTATGG	468
Oy	183	CysArgArgThrAspGluLeuValAspGlyProAlaAlaSerHisIleThrProGlnAla	202
Db	469	TGCAGAAACACAGATGAACTTGTTGATGGCCCAACGCATCATATTTATACCCGGCAGCG	528
Oy	203	LeuAspArgTrpGluThrArgLeuGlnAspLlePheSerGlyArgProPheAspMetLeu	222
Db	529	CTAGATAGGTGGGAAATAAGCTAAGATGCTTTCAATGGCGCGCCATTGTACATGTCTC	588
Oy	223	AspAlaAlaLeuSerSerAspThrValSerArgPheProValAspLleGlnProPheArgAsp	242
Db	589	GATGGCTCTTGTCCGATACAGTTCCTTAACTTCCAGTTGATTAATTCAGCATTCAGAGAT	648
Oy	243	MetLleGluGlnMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeu	262
Db	649	ATGATGTGAAGCAATCCGATATGACCTTGAGAAATACGAGATACAAAACCTTCACGCACTA	708
Oy	263	TyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly	282
Db	709	TACCTTTATGTTATTATATGTTGCTGTGACGTTGGTGTGATGATGAGTTCCAATTATGGGT	768
Oy	283	IleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGly	302
Db	769	ATCGCCCTGATCAAGGCAACACAGAGACCGTATATTAATGCTGTGGCTCTGGGG	828
Oy	303	LeuAlaAsnGlnLeuThrAsnLleLeuArgAspValGlyGluAspAlaArgArgGlyArg	322
Db	829	ATCGCAATTCATTAACATACACTCTCAGAGATGTTGGAGAAAGATGCCGAAGAGAGACA	888
Oy	323	ValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspLlePheAla	342
Db	889	GCTACTTGCCCTCAAGATGAATTAGACACGACGAGCTATCCGATGCAATATATTGGCT	948
Oy	343	GlyArgValThrAspLysThrArgAsnPheMetLysGlnIleGlnArgAlaArgLys	362
Db	949	GGAAAGGGGACCGAATTAATGAGAAATCTTTATGAAGAAACAAATCAATGGGCAAGAAAG	1008
Oy	363	PhePheAspGluSerGlnYsGlyValThrGluLeuAspSerAlaSerArgTrpProVal	382
Db	1009	TTCTTTGATGAGGCACAGAAATGGCGTGCACAGAAATTGAGTCACTATATTCCTGTA	1068
Oy	383	LeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluLleGlnAlaAsnAspTyrAsn	402
Db	1069	TGGCGATCTTGTGCTGTGACCGCAAAATATCATATGATGATTGAAGCAATGACTATCAAC	1122
Oy	403	AsnPheThrArgArgAlaTyrValSerLysProLysLeuLeuThrLeuProIleAla	422
Db	1129	AACTTCACAAAGAGAGCATATGTGAGCAAAATCAAAAGAAAGTTATGACATTACCTATGGCA	1188
Oy	423	TyrAlaLysSerLeuValProProAsnArgThrSerSer	435
Db	1189	TATGCAAAATCTCTGTGCTCTCTCAAAAACCTGCTCT	1227

```

XX 22-OCT-2002 (first entry)
XX
XX Tomato phytoene synthase cDNA.
XX
XX Gibberellin; transgenic plant; seed germination; seedling growth;
XX transgenic; phytoene synthase; enzyme; GA; gene; tomato; ss.
XX
XX Lycopersicon esculentum.
XX
XX Key Location/Qualifiers
XX CDS 1..1239
XX FT /*tag= a
XX FT /product= "Phytoene synthase"
XX FT /transl_except= (pos:1027..1029, aa:Lys)
XX FT /transl_except= (pos:1057..1059, aa:Arg)
XX
XX US2002053095-A1.
XX
XX 02-MAY-2002.
XX
XX 10-AUG-1999; 99US-0371307.
XX
XX 10-AUG-1999; 99US-0371307.
XX
XX (BROW/) BROWN S M.
XX
XX Brown SM, Ellich TD, Heck GR, Kishore GM, Logusch EM, Logusch SJ;
XX Piller KO, Rao S, Ream JE;
XX
XX WPI: 2002-489107/52.
XX P-PSDB; AAE24923.
XX
XX Control of gibberellin levels in plants useful to avoid unfavorable
XX conditions in crops to increase yields, using transgenic plants having
XX reduced seed germination and early seedling growth then treatment to
XX restore these properties
XX
XX Claim 45; Page 99; 155pp; English.
XX
XX The invention relates to control of gibberellin (GA) levels in plants.
XX The method involves producing transgenic plants having a phenotype
XX of reduced seed germination and reduced early seedling growth, then
XX restoring seed germination and early seedling growth by treating
XX plants with an appropriate compound when conditions are favourable.
XX The method is useful to control seed germination and/or early seedling
XX growth in agricultural production so that unfavorable environmental
XX conditions normally reducing agronomic output can be avoided and
XX yields increased. Plants also demonstrate increased uniformity of
XX germination, emergence and seedling vigor, so increasing yields at
XX harvest. The method is especially useful in crop plants such as e.g.
XX carotid, soybean, cotton, etc., and is also useful in storage and
XX transport of seeds to reduce premature germination which may affect
XX agronomic or food quality of the seeds. The present sequence is
XX tomato phytoene synthase cDNA. This cDNA is used in exemplification
XX of the invention.
XX
XX Sequence 1239 BP; 376 A; 208 C; 316 G; 339 T; 0 other;
XX
XX Alignment Scores:
XX Pred. NO.: 7.76e-177 Length: 1239
XX Score: 1737.00 Matches: 342
XX Percent Similarity: 86.37% Conservative: 32
XX Best Local Similarity: 78.98% Mismatches: 35
XX Query Match: 76.52% Indels: 24
XX Gaps: 3
XX
XX US-09-847-081B-2 (1-440) x AAD40272 (1-1239)
XX
XX 3 MetSerValAlaIleuLeuTPrpValValSerProThSerGluValSerAsnGlyThrGly 22
XX 1 ATGCTGTTGCTGCTGTTATGAGGTTGTTCTCCT--TGTGACGCTCTCAATGGACAACT 57

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QY	23	LeuLeuAaPSeSvAlaArgGIuGIyAaNaArgValPheValSeSeSArgPheLeuAlaArg	42
Db	58	TTCAATGAAATAGCTCCGGAGGAAACCGCTTTTTCATATCC-----AGG	105
QY	43	AspArgAaLeuMeTTrpAsnGIyArgIleuIySylGIyArgIlaArgTrpAsnDhe	62
Db	106	CATAGGAATTGGTGTCCAAATGAGAAATCAATAGAGT-----144	
QY	63	GlySerIleuIleAlaSPProArgTrpSerCysIleuGIyGlySerArgThGIuIySylGI	82
Db	145	-----GGTGAAGAACCAACTAATATGGA168	
QY	83	SeTrhPheSeSvAlGISeSerIeuValAlaSerProAlaGIuMeTThValSer	102
Db	169	CGAAATTTCTGTAAGGCTGCTGCTATTTGGCTACTCCATCTGGAGAACGGACGTATGACA228	
QY	103	SerGIuIySylSvAlTrpAspValValLeuIySgnAlaAlaLeValIySArgSIlneu	122
Db	229	TCGGAAACAGAGGTATGATAGTGTGTTTGAAGCAGGACGCTTGTAAGAGCGCACTG288	
QY	123	ArgSerThraSPaSPLeuGIuValIySPProAspIleValProGIyAaSIleuGIyIleu	142
Db	289	AGATCTACCAATGAGTTGAAAGTGAAGCCGATATCACTATTCGGGAAATTGGGCTTG348	
QY	143	LeuSerGIuAlaTrpAspArgCysGIyGIuValCysAlaGIuTrpAlaIySArgPheTrp	162
Db	349	TTGATGAGAACATGATAGTGGTGTGTAAGATATGTGACAGTATGCAAGACGTTTAC408	
QY	163	LeuGIyThrIySLeuMeTThProGIuArgArgAlaIleTrpAlaIleTrpAlaIleTrp	182
Db	409	TTAGGAATTAATGCTATATGACTCCGACAGAAAGAGGCGTATCTGGGCAATATATATG468	
QY	183	CysArgArgThraSPGIuIeuValaSPGIyProaAlaIaSerHisIleThProGIuAla	202
Db	469	TGCAGAAAGAACAGATGAACCTGTTGATGGCCCAACGCATATATATACCCGGCAGCC528	
QY	203	LeuAspArgTrpGIuThrArgIleuGIuAspIlePheSerGIyArgProPheAspMeIeu	222
Db	529	CTAGATAGGTGGGAAATAGGCTAGAAAGATGTTCAATGGGCGGCCATTGGACATGCTC588	
QY	223	AspAlaAlaIeLeuSerAspThrValSerArgPheProValaSPIleGIuProPheArgSP	242
Db	589	GATGGTCTTTGTCCGATACAGTTTCTAACTTTCCAGTTGATATTCAGCCATTGAGAAT648	
QY	243	MetIleGIuGIyMeArgMeCAspLeuTrpIySvSerArgTrpIySThPheAspGIuIeu	262
Db	649	ATGATTAAGAGAAATCGTATGAGACTTGAAGAAATGAGATCAAAAACTTGACAGCACTA708	
QY	263	TyrIleuTrpCysTrpTrpValAlaGIyThrValGIyLeuMeTSeSvAlProValMeGIy	282
Db	709	TACCTTTATTTGTATTATATGCTGGTGGTACGGTGGTGTGATGAGAGTGTCCAAATTAATGGGT768	
QY	283	IleAlaPProGIuSerIyAlaThThrGIuSeSvAlTyrAsnAlaIleuAlaIleuGIy	302
Db	769	ATCGCCCTGAATCAAGGCAACCAACAGAGCGATATATATATGCTTGGCTCTGGGG828	
QY	303	LeuAlaIeGIuIeuThraSPIleLeuArgAspValGIyGIuAspAlaArgArgGIyArg	322
Db	829	ATCGAAATTCATTAATCACTATCTCAGAGATGTGGAGAAAGATCCCAAGAGGAGAGA888	
QY	323	ValIyTrpLeuProGIuAspGIuIeuAlaGIuAlaGIyLeuSerAspGIuAspIlePheAla	342
Db	889	GTCATACCTGCTCAAGATGAATTAACACAGGCGAGCTATCCGATGAAGATATATTTGCT948	
QY	343	GIyArgValIleThraSPIySvAlaTrpArgAsnDheMetIySylSgnIleGIuArgAlaArgIyS	362
Db	949	GGAGAGGGAGCCGATTAATGGAGAACTTTTGAAGAAACAAATCATATGGGCAAGAAAG1008	
QY	363	PhePheAspGIuSerGIuIySylValThrGIuIeuAspSerAlaSerArgTrpProVal	382
Db	1009	TTCTTTTATGAGGCGAGAAATGGCGCTGACAGAAATTGACTCAGCTAGTATATTTCCCTGTA1068	
QY	383	LeuThraIleLeuIeuTrpArgIySIlleuAspGIuIleGIuAlaAsnAspTrpAsn	402

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QY 21 ThrGlyLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu 40
DB 252 ACAACCTTCATGAGATCACTCCGGAGGGAACCGTTTGGATTGATTCATCG----- 302
QY 41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgGlyLeuGlyGlyArgGlnArgTrp 60
DB 303 ---AGGCATAGAGAAATTTGGTGTCCCAATGAGAGAAATCAATAGAGGT----- 344
QY 61 AsnPheGlySerLeuIleAlaAspProArgTrpSerCysLeuGlyGlySerArgTrpGlu 80
DB 345 -----GGTGGAAAGCAAACTAT 362
QY 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThr 100
DB 363 AATGACGCGAAATTTCTGTAGCGTCTGTATTTGGCTACTCCATCTGGAGAACGGACG 422
QY 101 ValSerSerGluLeuValValTrpAspValValLeuGlyGlnAlaLeuValLysArg 120
DB 423 ATGACATCGAAGACAGATGGTCTATGATGTGTTTGAGGACGACCGCTTGGTGAAGAG 482
QY 121 GlnLeuArgSerThrAspAspLeuGluValLysProAspIleValValProGlyAsnLeu 140
DB 483 CAACAGATCTTACCAATGAGTTAGAGAGCGGATATACCTATTCGGGGAAATTTG 542
QY 141 GlyLeuLeuSerGluAlaTyrAspArgCysGlyGlyValCysAlaGlyTyrAlaLysThr 160
DB 543 GCGTTGTTAGAGGAGCATATGATAGTGTGTGAGAGTGTGCGAGATATGCCAAGACG 602
QY 161 PheTyrLeuGlyTyrThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIleTyr 180
DB 603 TTTAACTTAGGAACATGCTAATGACTCCCGAGAGAAAGGCGTATCTGTCATATAT 662
QY 181 ValTrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleLeuPro 200
DB 663 GTATGTCGAGAAAGACAGATGAACTGTGTGATGCCCAAGCAATATATTAATTAATCC 722
QY 201 GlnAlaLeuAspArgTrpGluThrArgLeuGluValAspIlePheSerGlyArgProPheAsp 220
DB 723 GCAGCCTTAGATAGTGGGAAATAGGCTAGAGAGATGTTTCAATGGCGGCCATTATAC 782
QY 221 MetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPhe 240
DB 783 ATGCTCGATGGTCTTTGTCCGATACAGTTTCTAATCTTCCAGTTGATATTCAGCCATTC 842
QY 241 ArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrAsp 260
DB 843 AGAGATATGATTTGAAGAGATGCGTATGACCTTGAGAGAAATCGAGATACAAAACCTTCAC 902
QY 261 GlnLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProVal 280
DB 903 GAACTATACCTTATTTATTTATTTATTTGTTGCTGAGCGTTGGGTTATAGAGTTCCATTT 962
QY 281 MetGlyIleAlaProGluSerLysValaThrThrGluSerValTyrAsnAlaAlaLeuVal 300
DB 963 ATGGGTATCGCCCTGGAATCAAGAGCAACACAGAGAGCGTATATTAATGCTGTGCTT 1022
QY 301 LeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuAlaGlyAspValGlyGluAspAlaArgArg 320
DB 1023 CTGGGATCGCAAAATCAATTAATCAATACATACAGATGTTGGAGAGATGCCGAGAGA 1082
QY 321 GlyArgValTyrLeuProGluAspGluLeuValGlnAlaGlyLeuSerAspGluAspIle 340
DB 1083 GGAGAGAGTCTACTTCCCTCAAGATGATTAATGACACGGAGCGTCTATCCGATGAGATATA 1142
QY 341 PheAlaGlyArgValThrAspLysTrpArgAsnPheMetLysValGlnIleGlnArgAla 360
DB 1143 TTTGCTGGAAGGCGTACCGATTAATGAGAAATCTTTATGAGAGAAACAAATACATAGGCA 1202
QY 361 ArgLysPhePheAspGluSerGlyLysGlyValThrGluLeuAspSerAlaSerArgTrp 380
DB 1203 AGAAGATCTTTGATGAGGACAGAGAAAGCGTGACAGAAATGAGCTCAGTATGATGTTTC 1262

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QY 381 ProValLeuThrAlaLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAsp 400
DB 1263 CCTGTATGGGAGATCTTTGGTCTGTACCGCAAAATACTAGTGAATTTGAAGCCAAATGAC 1322
QY 401 TyrAsnAsnPheThrArgAlaTyrValSerLysProLys-LysLeuLeuThrLeuPro 420
DB 1323 TACAAACAATTCACAAAGAGCATATGTGAGCAAAATCAAGCAAGATGATGATTAAC 1382
QY 420 GlnAlaTyrAlaLysSerLeuValProProAsnArgThrSerSerProLeuAlaLys 439
DB 1383 TATTGATATGCAAAATCTTGTGCTCTCT-----ACAAACTGCTCTCTTCAAA 1434

RESULT 13
AAV16951
ID AAV16951 standard; cDNA to mRNA; 2868 BP.
XX
AC AAV16951;
XX
DE 06-JUL-1998 (first entry)
XX
DE Nucleic acid encoding phycoene synthase 4.
XX
KM Phycoene synthase; breeding; variable flower colour; ds.
XX
OS Gentiana lutea.
XX
FH Key location/Qualifiers
FT CDS 400..1689
/*tag= a
FT
PV JP10084966-A.
XX
PD 07-APR-1998.
XX
PF 17-SEP-1996; 96JP-0245107.
XX
PR 17-SEP-1996; 96JP-0245107.
XX
PA (IWATE-) IWATE KEN.
XX
WP1: 1998-264853/24.
DR P-PSDB; AAW46964.
XX
PT Phytoene synthase gene - useful for breeding plant of variable
PT flower colour
PS Claim 4; Pages 12-14; 15pp; Japanese.
XX
CC The present sequence encodes phycoene synthase 4. It was isolated from
CC a cDNA library prepared from mRNA extracted from the petals of Gentiana
CC lutea. The nucleic acid sequence was amplified from the library using
CC PCR primers AAV16952-53. The phycoene synthase gene is useful for
CC breeding plants with variable flower colours.
XX
SQ Sequence 2868 BP; 887 A; 499 C; 648 G; 833 T; 1 other;

Alignment Scores:
Pred. No.: 4.98e-161 Length: 2868
Score: 1595.00 Matches: 313
Percent Similarity: 83.68% Conservative: 46
Best Local Similarity: 72.96% Mismatches: 60
Query Match: 70.26% Indels: 10
DB: 19 Gaps: 3

US-09-847-081B-2 (1-440) x AAV16951 (1-2868)
QY 1 MetSerMetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGly 20
DB 394 GTTAACTATGCTATTTTGTAGCGTATGGCTTTCCGCGAGTTCTGAAGTTTGAAGTGGC 453
QY 21 ThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu 40
DB 454 AATGTTTCTTGGAGCGCAATTCGAGAAAGT-----TACCAT 489

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QY 41 AlaArgSPaRgAsnLeuMetTrpAsnGlyArgGlyLeuLysGlyValArgGlnArgTrp 60
DB 490 TTTTCGGATAAAGTTTAAATGTCATGAGAGGTTAAGAAAGTGAACCAAGCGCT 549
QY 61 AsnPhenGlySerLeuLeuLeuAspProArgTrpSerCysLeuGlyGlySerArgTrpGlu 80
DB 550 AGATCAAGTTATGGGGTGAAGATTGAGTTCAATTTGCTTGAGAGAGCTGATAGAG 609
QY 81 ---LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMet 99
DB 610 ACCCGGGAGAGAAATTATCGGTATCTCCAGTATTATAGCTACCCGGAGAGAGAAAG 669
QY 100 ThrValSerSerGlyLysValArgValValLeuLysGlnAlaLeuValLys 119
DB 670 ACGATGACATCAGAGCAAAAGTTTATGATGCTTTTAAAGACACACCTTGATTAAT 729
QY 120 ArgGlnLeuArgSerThrAspAspLeuGluValLysProAspLleValProGlyAsn 139
DB 730 AGACAGTTGAGGCTTAGAGAAATTGGAGGTGAACCGGACATTAATTTGGCCAGGAAC 789
QY 140 LeuGlyLeuLeuSerGlnAlaTrpAspArgCysGlyGluValCysAlaGlyTrpAlaLys 159
DB 790 GCGAAGCTGTGATGATGAGCTTATGATCGGTGCGAGAGATGCTGATATATGCAAG 849
QY 160 ThrPheTrpLeuGlyThrLysLeuMetThrProGluArgArgAlaLleTrpAlaLle 179
DB 850 TCATTCTACTGGGGAAACCAAGCTCATGACACCGAGAGCGCTTTAGCTATCTGGGGATA 909
QY 180 TyrValTrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisLleThr 199
DB 910 TATGTATGTGTAGAGGAGCAGATGAGCTTGTTGAGGGCCCTPACCGCTACACATTAAT 969
QY 200 ProGlnAlaLeuAspArgTrpGluTrpArgLeuGluAspLlePheSerGlyArgProPhe 219
DB 970 CCACCGCGTGAATGAGTGGGAGCAAGCAATTGAAGAGTGTTCACAGGCAACCTTTT 1029
QY 220 AspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspLleGlnPro 239
DB 1030 GATATGCTTGAATGCTGCTTATCTGATACCATTAACCAAGTATCTTGACATCCAGCA 1089
QY 240 PheArgAspMetLleGluGlyMetArgMetAspLeuTrpLysSerArgTrpLysThrPhe 259
DB 1090 TTTAGAGATATGATAGAGAAATGCGGATGATCTGAAGAAATCGAGATCAAGATTTTC 1149
QY 260 AspGluLeuTrpLeuTrpCysTrpTrpValAlaGlyLysValGlyLeuMetSerValPro 279
DB 1150 GATGAGCTGTATCTTACTGCTAATTAATGCGCTGATCAGTTGGCTGATGATGATACCA 1209
QY 280 ValMetGlyLleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeu 299
DB 1210 GTATAGGAGATTCGACCTGAAATCTAAGGCAACAGAAAGTGTGATATGACAGCTTTA 1269
QY 300 AlaLeuGlyLeuAlaAsnGlnLeuThrAsnLleLeuArgAspValGlyLysAlaArg 319
DB 1270 TCTTTGGGATGCGGAGACCAAGCTGACTTAACATCTTAAGGAGAGTTGGAAGAAGTGA 1329
QY 320 ArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAsp 339
DB 1330 AAGAGGAGAGTGAACCTACCTCAAGATGAATTAGCAAGACGAGTTTATCAAGATGAGCA 1389
QY 340 IlePheAlaGlyArgValThrAspLysTrpArgAsnPheMetLysLysGlnLleGlnArg 359
DB 1390 ATTTTTCGTAAGAAATTCACAGCAATGAGAGATTTTATGAGAGAGCAAAATCAAAAG 1449
QY 360 AlaArgLysPhePheAspLysSerGlyLysGlyValThrGluLeuAspSerAlaSerArg 379
DB 1450 GCTAGAAATTCATGATGATGAGAGAGAGGTCCCGAATCAAGCTCCGGAAGACAG 1509
QY 380 TrpPro---ValLeuThrAlaLeuLeuLeuTrpArgLysLleLeuAspGluLleGlnAla 398
DB 1510 ATTGCTGTGTGGCCAGCGTTTGTCTTTTATAGAAAATATTTGATGATGATAGAGCA 1569

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QY 399 AsnAspTyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuThr 418
DB 1570 AATGACTACCAAAATTTTACAAAAGGCTTATGTAACCAAGGCAAGAGCTATTAGCT 1629
QY 419 LeuProLleAlaTyrAlaLysSerLeu 427
DB 1630 ATGCTGTGATGATGTCACAAAGTCTCTC 1656
RESULT 14
AAV16949
ID AAV16949 standard; cDNA to mRNA; 1921 BP.
XX
AC AAV16949;
XX
DT 06-JUL-1998 (first entry)
XX
DE Nucleic acid encoding phytoene synthase 2.
XX
KW Phytoene synthase; breeding; variable flower colour; ds.
XX
OS Gentiana lutea.
XX
FH Key Location/Qualifiers
FT CDS 412..1689
FT /*tag= a
PN JP10084966-A.
PD 07-APR-1998.
XX
PF 17-SEP-1996; 96JP-0245107.
XX
PR 17-SEP-1996; 96JP-0245107.
XX
PA (IMAT-) IMATE KEN.
XX
DR WPI; 1998-264853/24.
XX
DR P-PSDB; AAW46962.
XX
PT Phytoene synthase gene - useful for breeding plant of variable
PT flower colour
PS Claim 2; Pages 7-9; 15pp; Japanese.
XX
CC The present sequence encodes phytoene synthase 2. It was isolated from
CC a cDNA library prepared from mRNA extracted from the petals of Gentiana
CC lutea. The nucleic acid sequence was amplified from the library using
CC PCR primers AAV16952-53. The phytoene synthase gene is useful for
CC breeding plants with variable flower colours.
XX
SQ Sequence 1921 BP; 633 A; 236 C; 438 G; 554 T; 0 other;
Alignment Scores:
Pred. No.: 3,426-157 Length: 1921
Score: 1557.00 Matches: 305
Percent Similarity: 81.82% Conservative: 46
Best Local Similarity: 71.10% Mismatches: 68
Query Match: 68.59% Indels: 10
DB: Gaps: 2
US-09-847-081B-2 (1-440) x AAV16949 (1-1921)
QY 1 MetSerMetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGly 20
DB 406 GTTAACATGCTAATTTGTACGCTATGAGGTGTTTGGCCGAGTTCTGAAGTTTGTAGTGC 465
QY 21 ThrGlyLeuLeuAspSerValArgGlyLysAsnArgValPheValSerSerArgPheLeu 40
DB 466 AATGTTTCTTGAGCCCAATTGCAAGAGT-----TACCAT 501
QY 41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgGlyLysGlyValArgGlnArgTrp 60
DB 502 TTTTCGGATAAAGTTTAAATGTCATGAGAGGTTAAGAAAGTGAACCAAGAGCGCT 561

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QY 61 AsnphgIySerLeuIleAlaAspProArgTyrSerCysLeu-----GlyGlySerArg 78
DB 562 AGATACAGCTTATGGGCTTGAGATTGAGTTGATTTCTTCTTGAGAGAGCTGGATTAG 621
QY 79 ThrGluIySGlySerThrPheserValGlnSerSerLeuValAlaSerProAlaGlyGlu 98
DB 622 ACCCGGGAAGAAAGATTATCGGTTCCTCCAGATTAAATAGCTAACCCCGGCGAGAGA 681
QY 99 MetThrValSerSerGluIyLeuValTyrAspValValIleuValGlnAlaLeuVal 118
DB 682 ATGAGCATGACATCAGACAAAGGTTATGATGCTGTTTAAACAGACGACTTGATT 741
QY 119 LysArgGlnLeuArgSerThrAspAspLeuGluValLysProAspIleValValProGly 138
DB 742 AATGACAGCTTGAGCTTACAGAAATTTGAGAGTGAACCGGACATTATTTTGCACAGA 801
QY 139 AsnLeuGlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAla 158
DB 802 AACCGGAACGTGTGATGAAGCTTATGTCGTCAGAAATGATGTCGAATATGCTC 861
QY 159 LysThrPheTyrLeuGlyThrIleuMetThrProGluArgArgAlaIleTyrAla 178
DB 862 AAGTCATTCTCCTGAGGAAACCGCTCATGACACCGAGAGCGCTTACCTATCTGAGCG 921
QY 179 IleTyrValITPcysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIle 198
DB 922 ATATATGATGTGTGATGAGAGACAGATGAGCTGTGATGAGCTTAAAGCGCTCAACATA 981
QY 199 ThrProGlnAlaLeuAspArgTyrGluThrArgLeuGluValAspIlePheSerGlyValArgPro 218
DB 982 AATCCAAACCGGCTTATGATGAGTGGAGACAGATTAGAAAGTGTTCAAAGGCGCAACT 1041
QY 219 PheAspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGln 238
DB 1042 TTGTATATGCTTGAATGCTGCTTATCTGATACCATTCACATATCTGTCGACATCCAG 1101
QY 239 ProPheArgAspMetIleGluGlyMetArgMetAspLeuTyrLysSerArgTyrLeuThr 258
DB 1102 CCATTATGAGATGATGATGAAGAGATGCGGATGATCTGAAGAAATCCAGATACAGAGAT 1161
QY 259 PheAspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerVal 278
DB 1162 TTCGATGAGCTGATCTTACCTGATATGTCGTCGATGAGTGGCTGATGATGCTGA 1221
QY 279 ProValMetGlyIleAlaProGluSerLysAlaThrThrGlnSerValTyrAsnAlaIle 298
DB 1222 CCAGTAAATGGCATTTGACCTGAATCTAAGSCAACAGAAAGTGTATATATACACT 1281
QY 299 LeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAla 318
DB 1282 TTATCTTTGGGAGATGCCAACACAGCTGATTAACATTTCAAGGAGCTTGGAGAAATGCA 1341
QY 319 ArgArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGlu 338
DB 1342 AGAAGAGAGAGAGTGTACCTACCTCAAGATGATAGCAACAGAGCTTATACATGAG 1401
QY 339 AspIlePheAlaGlyArgValThrAspLysTyrPheAsnPheMetLysLysGlnIleGln 358
DB 1402 GACATTTTTCGTAAGAAAGTTACAGACAAATGAGAGATTTTATAGAAAGCAAAATCAAA 1461
QY 359 ArgAlaArgLysPheAspGlnSerGluValAlaThrGluLeuAspSerAlaSer 378
DB 1462 AGGGCTAAGAAATTTATGATGATGACAGAAAAAAGTCCCCCGAACTCAGCTCCGCGAGC 1521
QY 379 ArgTyrProValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAla 398
DB 1522 AGATTGCTGTGTGGGACGCTTGTCTTTATAGAAAAATTTGAGATGAGATTAACAGA 1581
QY 399 AsnAspTyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThr 418
DB 1582 AATGACTACAAACAAATTTCACAAAAAGGGCTTATGTAAACAAAGCAAGAGACTTATAGCT 1641

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QY 419 LeuProIleAlaTyrAlaLysSerLeu 427
DB 1642 ATGCTGATGACATGTCCTCTCTC 1668

RESULT 15
AB212924
ID AB212924 standard; DNA, 1269 BP.
AC AB212924;
XX 21-JAN-2003 (first entry)
DT
XX Arabidopsis thaliana stress regulated gene SEQ ID NO 729.
DE
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX Arabidopsis thaliana.
XX
XX MO200216655-A2.
XX
XX 28-FEB-2002.
XX
XX 24-AUG-2001; 2001WO-US26685.
XX
XX 24-AUG-2000; 2000US-227866P.
XX 26-JAN-2001; 2001US-264647P.
XX 22-JUN-2001; 2001US-300111P.
XX
XX (SCRI ) SCRIPPS RES INST.
XX (SYGN ) STINGENTA PARTICIPATIONS AG.
XX
XX Harper JF, Krebs J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
XX
XX Identifying a stress condition to which a plant cell has been exposed
XX and producing plants with increased tolerance to these abiotic stresses
XX
XX Claim 144; SEQ ID NO 729; 577bp + Sequence Listing; English.
XX
XX The invention relates to identifying a stress condition to which a plant
XX cell has been exposed, comprising:
XX (a) contacting nucleic acid representative of expressed polynucleotides
XX in the plant cell with an array or probes representative of the plant
XX cell genome; and
XX (b) detecting a profile of expressed polynucleotides in the plant cell
XX characteristic of a stress response. The method is useful in the
XX production of transgenic plants, cells and seeds and in producing plants
XX with increased tolerance to abiotic stress. The present sequence is that
XX of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
XX in methods of the invention.
XX Note: The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied to Derwent by
XX the European Patent Office.
XX
XX Sequence 1269 BP; 365 A; 230 C; 315 G; 359 T; 0 other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 7.71e-156 Length: 1269
XX Score: 1542.00 Matches: 318
XX Percent Similarity: 81.86% Conservative: 43
XX Best Local Similarity: 72.11% Mismatches: 51
XX Query Match: 67.93% Indels: 30
XX DB: 24 Gaps: 8
XX
XX US-09-847-081B-2 (1-440) x AB212924 (1-1269)
QY 1 MetSerMetSerValAlaLeuLeuTyrValVal-----SerProThrSerGluValSer 18
DB 1 ATGCTTCTTCTTGAAGAGGTTATGAGTCTTCTTCTTAATCCAGACCCCAATG 60
QY 19 AsnGlyThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArg 38

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OM protein - nucleic search, using frame_plus.p2n model

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2339.862 Million cell updates/sec

Title: US-09-847-081B-2

Perfect score: 2270

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Delop 6.0	Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1799	79.3	1814	1	US-08-579-667-7
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4	1762	77.6	1316	1	US-08-579-667-3
5	1750	77.1	1239	3	US-09-180-342-2
6	1744	76.8	1239	3	US-09-180-342-1
7	1732	76.3	1646	1	US-07-995-950-2
8	1732	76.3	1646	1	US-08-300-582-2
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13	364	16.0	1198	1	US-08-096-623A-5
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22	326	14.4	11233	3	US-08-980-833-27
23	324	14.3	908	3	US-08-660-645A-4
24	324	14.3	908	3	US-09-298-718-4
25	324	14.3	908	3	US-09-546-965-4
26	293	12.9	536165	4	US-09-214-808-1
27	176.5	7.8	947	1	US-08-096-623A-16
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29	174	7.7	2470	4	US-09-091-725-18
30	174	7.7	2546	4	US-09-091-725-12
31	170	7.5	405	3	US-09-060-755-345
32	170	7.5	405	4	US-09-670-314-345
33	159	7.0	3550	4	US-09-091-725-22
34	136.5	6.0	2054	1	US-08-351-981-1
35	121	5.3	1349	1	US-08-351-981-5
36	120	5.3	1326	4	US-09-625-188-3
37	116	5.1	1642	1	US-08-310-693-1
38	116	5.1	1642	5	PCT-US95-11280-1
39	112.5	5.0	114	2	US-08-260-546-10
40	112.5	5.0	114	4	US-09-436-068A-12
41	112.5	5.0	114	4	US-09-265-576-12
42	111.5	4.9	346	3	US-09-060-755-427
43	111.5	4.9	346	4	US-09-670-314-427
44	108	4.8	39195	4	US-08-311-731A-133
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ALIGNMENTS

RESULT 1
US-08-579-667-5
Sequence 5, Application US/08579667
Patent No. 5705624
GENERAL INFORMATION:
APPLICANT: Filizmaurice, Wayne P.
APPLICANT: Hellmann, Gary M.
APPLICANT: Grill, Laurence K.
APPLICANT: Kungel, Monto H.
TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
PHYTOENE BIOSYNTHESIS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia C. Bennett
STREET: 1211 East Morehead Street, PO Drawer 34009
CITY: Charlotte
STATE: No. 5705624th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,667
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET INFORMATION: 627-196
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1826 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 367..1596
US-08-579-667-5

Alignment Scores:
Pred. No.: 3,226-204 Length: 1826
Score: 1826.00 Matches: 362
Percent Similarity: 88.61% Conservat: 27
Best Local Similarity: 82.46% Mismatches: 21
Query Match: 80.44% Indels: 29
DB: 1 Gaps: 4

US-09-847-081B-2 (1-440) x US-08-579-667-5 (1-1826)

QY	3	MetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGlyThrGly	22
DB	367	ATGCTCTGTTGCTTGTATGGGTGTTTCACCT--TGAGAGTCTCAAAATGGGACAGGA	423
QY	23	LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg	42
DB	424	TTCTTGATTCGTAAGGAGGAGAAACCGGCTTTTGACTGCTCG-----AGG	471
QY	43	AspArgAsnLeuMetTrpAsnGlyArgIleuLysGlyGlyArgIleuArgTrpAsnPhe	62
DB	472	CATAGGAATTATGATGTCATGAGATCAAAAGAGGTGTAACAAAGGATGGAATTTT	531
QY	63	GlySerLeuIleAlaAspProArgTrpSerCysLeuGlyGlySerArgThrGluLysGly	82
DB	532	GGT-----	534
QY	83	SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMet---ThrVal	101
DB	535	-----TCGTACGGCTGCGATGGTGGCTACCAACCGGAGAAATGGCCAGCAATG	585
QY	102	SerSerGluLysLysValTyrAspValValLeuLysGlnAlaLeuValLysArgGln	121
DB	586	ACATACAGAACAGAAAGTTATGATGCTGATTTGAACAACAGCCTTGTGTAAGGACAG	645
QY	122	LeuArgSerThrAspAspLeuGluValLysProAspIleValProGlyAsnLeuGly	141
DB	646	CTGAGATCTACTGATGATTTGAAAGTGAACCGGAGATCCCTCCCGGGAATTTGAGC	705
QY	142	LeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPhe	161
DB	706	TTGTTTAAGTGAAGCATATGATAGTGTAGTGAAGTATGGCAGATATGCAAAAGCATTT	765
QY	162	TyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIleTyrVal	181
DB	766	TACTTAGGAACATATGCTATATGACTCTCAGAGAGAAAGGCGATTTGGGCATATATCTA	825
QY	182	TrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGln	201
DB	826	TGGTCACAGAGAACATGATGAACCTGTTGATGCCCCGAAATGCATCATATTAATCTCAAA	885
QY	202	AlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMet	221
DB	886	GCCTTAGATAGGTGGGAAAGACCGGCTGGAAGATGTTTTCAGTGGCGGCATTGATATG	945
QY	222	LeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArg	241
DB	946	CTCGATGCTGCTTTTCCGATATCTGTTTCCAGTTTCCAGTTGATATTCAGCGCTTCAGA	1005
QY	242	AspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGlu	261
DB	1006	GATATGATTTGAAGGAATCGGTATGACTTGAAGAAAGTCAAGATACAGAAACCTTTGATAG	1065

QY 262 LeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMet 281
DB 1066 CTATACCTATATTTCTTATTTACGTTGCTGTAACGTTGGTTGATGATGTTCCAAATATATG 1125
QY 282 GlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeu 301
DB 1126 GGTATTCACCTGATTCAAAGGCAACAGAGAGTATATATATATGACGCTTTGGCTTTA 1185
QY 302 GlyLeuAlaAsnGluLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGly 321
DB 1186 GGGATCGCAATCAACTACCAACATATCTCAGATATTCGAGAGATGCGAGAAAGAGGA 1245
QY 322 ArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePhe 341
DB 1246 AGAGTCTACTTACTCTCAAGATGATTTAGCACAGCAGAGTCTCTCCGCAATGACATTTT 1305
QY 342 AlaGlyArgValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaArg 361
DB 1306 GCTGGAAGAGTACTGATTAATATGAGAAAGCTTTATGAAGAAAGCAATCCAGAGGCAAGA 1365
QY 362 LysPhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrpPro 381
DB 1366 AAATTTCTTCACAGAGGAGAGAGAGTACACACTGAGCTGACTAGATGATGCT 1425
QY 382 ValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyr 401
DB 1426 GTATGGGATCTTTGCTGCTGTATACCCGACAGATCTGACAGATGTAAGCAATGACTAC 1485
QY 402 AsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuProIle 421
DB 1486 AACCACTTCACAGAGAGAGCTTATGTAGCAAAACCAAGAAAGCAATTCCTTACCTAAT 1545
QY 422 AlaTyrAlaLysSerLeuValProProAsnArgThr-SerSerProLeuAlaLys 439
DB 1546 GCTTATGCAAAATCTTGTGCCCCCTTACAAAGAACTCTTGACCTTACCTAGCTAAG 1600

RESULT 2
US-08-579-667-7
Sequence 7, Application US/08579667
Patent No. 5705624
GENERAL INFORMATION:
APPLICANT: Filizmaurice, Wayne P.
APPLICANT: Hellmann, Gary M.
APPLICANT: Grull, Laurence K.
APPLICANT: Kumagai, Monto H.
APPLICANT: Della-Cioppa, Guy R.
TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Virginia C. Bennett
STREET: 1211 East Morehead Street, PO Drawer 34009
CITY: Charlotte
STATE: No. 5705624th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,667
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 627-196
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175

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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1814 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 363..1592
US-08-579-667-7

Alignment Scores:
  Pred. No.: 4,71e-201      Length: 1814
  Score: 1799.00           Matches: 356
  Percent Similarity: 87.93% Conservative: 30
  Best Local Similarity: 81.09% Mismatches: 24
  Query Match: 79.25%      Indels: 29
                        Gaps: 4

US-09-847-081b-2 (1-440) x US-08-579-667-7 (1-1814)

QY      3 MetSerValAlaLeuLeuTyrValValSerProThrSerGluValSerAsnGlyThrGly 22
DB      363 ATGTCGTGCTGCTGTTATGAGGTTGTCACCT--TGTGAAGCTCCAAATGGACAGCA 419

QY      23 LeuLeuAspSerValArgGluGlyAsnArgValLpheValSerSerArgPheLeuAlaArg 42
DB      420 TTCCTTGATTCAGTCCGGAGGGAACCGGGATTTTGATTGCTGC-----AGG 467

QY      43 AspArgAsnLeuMetTyrAsnGlyArgGlyLeuGlyGlyArgGlnArgTyrAsnPhe 62
DB      468 CATAGAAATTATGTGTGCAATGAGAAACAAGAGAGGTGTAACAAAGTGGAAATTTT 527

QY      63 GlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluGly 82
DB      528 GGT----- 530

QY      83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMet---ThrVal 101
DB      531 -----TCTGTAAGGCTCTGTAAGGCTACACCGCGGAGAAATGGCGACGAG 581

QY      102 SerSerGluValLeuValTyrAspValValLeuValGlnAlaLeuValIleValArgGln 121
DB      582 ACATCAGAACAGATGTTATGATGCGCTTTAAACAAGCAGCTTATGAGAGCGAG 641

QY      122 LeuArgSerThrAspAspLeuGluValIleProAspIleValValProGlyAsnLeuGly 141
DB      642 TTGAATCTGCTGATGATTTAGAGTGAAGCCGAGATCCTCTCCCGGAATTTGAGC 701

QY      142 LeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaIleThrPhe 161
DB      702 TTGTTGAGGAGAACATGATGATGAGTGTAGTGAAGTATGACAGATGCCAAGACATT 761

QY      162 TyrLeuGlyThrIleLeuMetThrProGluArgArgAlaIleTyrAlaIleTyrVal 181
DB      762 TACTTAGAACACATGCTATGACTCCAGAGAGAAAGGCTATTGGGCATATATG 821

QY      182 TyrCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGln 201
DB      822 TGGTCACAGAGAACATGATGATGCTGTTGAGCCCAAGCATCATGTTACACCCCA 881

QY      202 AlaLeuAspArgTyrGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMet 221
DB      882 GCTTAGAGTGGGAGAACCGGCTTGAAGATGTTTCAAGGGGACATTGTATG 941

QY      222 LeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArg 241
DB      942 CTCGATGCTGCTGTTGCCATGCTGTTCCAGCTTCCAGCTTCAATATGACCGCTTCA 1001

QY      242 AspMetIleGluGlyMetArgMetAspLeuTyrIleSerArgTyrIleThrPheAspGlu 261
DB      1002 GATATGATTGAAGAAATCGGTATGACTTGAAGAACTCAAGATATATGAACCTTTGATG 1061

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QY      262 LeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMet 281
DB      1062 CTTTACCTCTATGTTATTAAGCTTCTGCTACCGTGGCTTGATGATGACGCTTCCATTATG 1121

QY      282 GlyIleAlaProGluSerIleAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeu 301
DB      1122 GGTATTTGACCTGATTTCAAGGCAACAACAGAGAGCTATATATGACGCTTGCTTTA 1181

QY      302 GlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGly 321
DB      1182 GGAATCGGAATCAACTACAGCAACTACTCAGGAGTTTGAGAAAGATGCCAAGAGCA 1241

QY      322 ArgValTyrLeuProGluAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePhe 341
DB      1242 AGAGCTCTATTCCTCAAGATGAAATTAACACAGGAGGCTCTTGGACGATGATATTT 1301

QY      342 AlaGlyArgValThrAspLysTyrAsnPheMetLysGlnIleGlnArgAlaArg 361
DB      1302 GCTGGAAGAGTACATGATTAAGTGAAGAGCTTTATGAAGAAGCAATCCAGAGGCAAGA 1361

QY      362 LysPhePheAspGluSerGluGlyValThrGluLeuAspSerAlaSerArgTyrPro 381
DB      1362 AAGTCTTCGATGAGGCAAGGAGGAGGAGTTACACAACTGAGCTCAGTACAGATGGCT 1421

QY      382 ValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyr 401
DB      1422 GTATGGGATCTTCTGCTGTTGTCACCAATATCTGACGAGATTTGAAGCCATATACATC 1481

QY      402 AsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuProIle 421
DB      1482 AACACTTCACAAAGAGCTTATGATGAGCAAAACCAAGAAAGCTTATTCCTTACCTATT 1541

QY      422 AlaTyrAlaLysSerLeuValProProAsnArgThr-SerSerProLeuAlaLys 439
DB      1542 GCTTATGAAAATCTCTGTGCCCCCTTCAAGAACTTGTCACTTGAAGCTTAAG 1596

RESULT 3
US-08-579-667-1
; Sequence 1, Application US/08579667
; Patent No. 5705624
; GENERAL INFORMATION:
; APPLICANT: Filizmaurice, Wayne P.
; APPLICANT: Hellmann, Gary M.
; APPLICANT: Grill, Laurence K.
; APPLICANT: Kumagai, Monto H.
; APPLICANT: Della-Cioppa, Guy R.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia C. Bennett
; STREET: 1211 East Morehead Street, PO Drawer 34009
; CITY: Charlotte
; STATE: No. 5705624th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,667
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 627-196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175

```

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1795 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 362..1591
 US-08-579-667-1

Alignment Scores:

Score:	3.98e-198	Length:	1795
Percent Similarity:	1774.00	Matches:	351
Best Local Similarity:	87.07%	Conservative:	33
Query Match:	79.59%	Mismatches:	28
	78.15%	Indels:	29
		Gaps:	4

US-09-847-081b-2 (1-440) x US-08-579-667-1 (1-1795)

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Qy 1 MetSerMetSerValAlaLeuLeuTyrValAlaSerProThrSerGluValSerAsnGly 20
Db 356 CTCAGAAATGCTGCTGCTTGTATGGGTGTTTCACCT--TGTGAGGTCTCAATGGG 412
Qy 21 ThrGlyLeuLeuAspSerValArgGluGluValAsnArgValPheValSerArgPheLeu 40
Db 413 ACAGATATCTTGATTCATTTCGGAGGGAACCCGGTTTGTGATTGTCAGAGTAT-- 469
Qy 41 AlaArgAspArgAsnLeuMetTyrAsnGlyValGlyLeuValArgGlyValArgGlyTyr 60
Db 470 -----AGAAATTTAGTGTGCAATGAGAGCAACAGAGAGGTGGGAAACAAAGGTGG 520
Qy 61 AsnPheGlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGlu 80
Db 521 AATTTTGGT----- 529
Qy 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMet--- 99
Db 530 -----TCTGTAGGCTCTGCTATGCTGCTACACCGCGCGAGAAATGGCG 574
Qy 100 ThrValSerSerGluValLysValTyrAspValValLeuValGlnAlaLeuValLys 119
Db 575 ACGATGACATCAGAACACATGCTTATGATGCTTTAAACAGACGCTTATGAG 634
Qy 120 ArgGluLeuArgSerThrAspAspLeuGluValLysProAspIleValProGlyAsn 139
Db 635 AGCGAGTTGAGATCTACTGATGATTTAGAGGAGCCGAGATCCTCTCCAGGCAAT 694
Qy 140 LeuGlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLys 159
Db 695 TTGAGCTTGTGAGGAGCAATGATGATGAGTGTAGTGAAGATGTCAGAGATGCAAG 754
Qy 160 ThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgArgAlaIleTyrAlaIle 179
Db 755 ACATTTTACTTACGAGAACCATGCTATGACTCCAGAGAGAGAGAGGCTATTGGGCATA 814
Qy 180 TyrValTyrCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThr 199
Db 815 TATGATGTCGACGAGAGAACAGATGATGCTTGTGATGCGCCGAAATGCCATATTATTC 874
Qy 200 ProGlnAlaLeuAspArgTyrGluThrArgLeuGluAspIlePheSerGlyValArgProhe 219
Db 875 CCACAAAGGCTTAGAGATGGTGGGAAAGACCTGCTGGAAGATGTTTTCAGTGGCGGCATT 934
Qy 220 AspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnPro 239
Db 935 GATATGCTCGATGCTGCTTGTTCATCTGTTTCCAGTTTCCAGTTTCAATTATTCAGCCA 994
Qy 240 PheArgAspMetIleGluGlyMetArgMetAspLeuTyrLysSerArgTyrLysThrPhe 259
Db 995 TTCAGAGATATGATTTGAAGAAATGCGTATGACTTGAAGAAAGTCAAGATACAGAAACTTT 1054

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Qy 260 AspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValPro 279
Db 1055 GATGAGCTATACCTATATTTGTTATTTACCTGCTGCTGACGGTGGGCTTGAAGCTTCCA 1114
Qy 280 ValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeu 299
Db 1115 ATTATGGGATTTGACCTGATTCAGTCAAGCAACAGAGATGATATATATGCGCTTTG 1174
Qy 300 AlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyLysAspAlaArg 319
Db 1175 GCTTGGGTATAGCAAAATCAACTAACAACTACTCAGAGATGTCGAGAGAGATGCCAGA 1234
Qy 320 ArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAsp 339
Db 1235 AGAGAAAGAGCTTACTTACTCAAGATGATTTAGACATGACAGGTCTCTCCAGAGATGAC 1294
Qy 340 IlePheAlaGlyArgValThrAspLysTyrArgAsnPheMetCysLysGlnIleGlnArg 359
Db 1295 ATATTTCCTGGAAGAAAGTGAAGAGATTAATGAGAAAGCTTTATGAAAGAACAAATCCAGAG 1354
Qy 360 AlaArgLysPhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArg 379
Db 1355 GCAAGAAAGTTCCTTGTATGAGGCGAGAGAGAGAGTGAACAACCTGACCTCAGCTAGTAGA 1414
Qy 380 TyrProValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsn 399
Db 1415 TGACCTGATAGCGCTTCTTGTCTGTTTACCGCAAGTACTCCAGAGATGAGAGCCAT 1474
Qy 400 AspTyrAsnAsnPheThrArgArgAlaTyrValSerLysProIlyLysLeuLeuThrLeu 419
Db 1475 GACTACAAACAATTCACAAAGAGAGCTTATGTGAGCAAAATCAAGAAAGCTAATTCCTTA 1534
Qy 420 ProIleAlaTyrAlaLysSerLeuValProProAsnArgThrSerSerProLeuAlaLys 439
Db 1535 CCAATTCATATGCAAAATCTTGTGCCCCCAACAAGAACTTGTCTCTCCTAGCTAA 1594
Qy 439 s 439
Db 1595 G 1595

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RESULT 4
 US-08-579-667-3
 Sequence 3, Application US/08579667
 Patent No. 5705624
 GENERAL INFORMATION:
 APPLICANT: Fitzmaurice, Wayne P.
 APPLICANT: Hellmann, Gary M.
 APPLICANT: Grill, Laurence K.
 APPLICANT: Kumagai, Monto H.
 APPLICANT: Della-Cioppa, Guy R.
 TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
 NUMBER OF SEQUENCES: 19
 TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Virginia C. Bennett
 STREET: 1211 East Morehead Street, PO Drawer 34009
 CITY: Charlotte
 STATE: No. 5705624th Carolina
 COUNTRY: USA
 ZIP: 28234
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/579,667
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Bennett, Virginia C.
 REGISTRATION NUMBER: 37,092

REFERENCE/DOCKET NUMBER: 627-196
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-420-2200
 TELEFAX: 919-881-3175
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1316 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1239
 US-08-579-667-3

Alignment Scores:

Pred. No.:	6,18e-197	Length:	1316
Score:	1762.00	Matches:	347
Percent Similarity:	87.04%	Conservative:	29
Best Local Similarity:	80.32%	Mismatches:	28
Query Match:	77.62%	Indels:	28
DB:	1	Gaps:	4

US-09-847-081B-2 (1-440) x US-08-579-667-3 (1-1316)

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QY      3 MetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGlyThrGly 22
DB      1 ATGCTGTGCTGCTTTATGAGTGTGTTTCACT---TGTGAGGTCTCAATATGGAACGGA 57
QY      23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42
DB      58 TTCTTGATTCATCATCCGGAGGGAACCGGGTTTGTGATGTGTCG-----AGG 105
QY      43 AspArgAsnLeuMetTrpAsnGlyArgGlyLeuGlySerGlyGlyArgGlnArgTrpAsn 62
DB      106 CATAGAAATTTAGTGTGATGATGAGAAACAGAGAGGTGTGAAACAATGTGGAATTTT 165
QY      63 GlySerLeuLeuAlaAspProArgTrpSerCysLeuGlyGlySerArgThrGluLeuGly 82
DB      166 GGT----- 168
QY      83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMet---ThrVal 101
DB      169 -----TCTGTAAGCTGCTGTATGATGCTACACCGCGGGAATGCGCAGCATG 219
QY      102 SerSerGluGlyValValValValValValValValValValValValValValValVal 121
DB      220 ACATCAGAACAGATGCTTATGATGTGATGATGAAACAAACAGCTTTAGTGAAGAGCAG 279
QY      122 LeuArgSerThrAspAspLeuGluValValProAspIleValValProGlyValAsnLeuGly 141
DB      280 TTGACATCTACTGATGATTTTGAAGTGAAGCGCGAGATCCCTCCCGGGGAATTTGAGC 339
QY      142 LeuLeuSerGluValValValValValValValValValValValValValValValVal 161
DB      340 TTGTTGATGGAAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 399
QY      162 TyrLeuGlyThrValLeuMetThrProGluArgArgValAlaIleTyrAlaIleTyrVal 181
DB      400 TACTTAGAGAACTATGCTATGACTCCAGAGAGAAAGAGGCTATTGGGCAATATATGTA 459
QY      182 TrpCysArgArgThrAspGluLeuValAlaAspGlyProAsnAlaSerHisIleThrProGln 201
DB      460 TGGTGACAGAGAACAGAGAACTTGTGATGCGCCGAAATGCAATATATATATATATATAT 519
QY      202 AlaLeuAspArgTrpGluThrArgLeuGluValAlaIlePheSerGlyArgProPheAspMet 221
DB      520 GCTTTAGATAGTGGTGAAGACCGGCTGGAAGATGTTTCAAGTGGCGGCATTTGACATG 579
QY      222 LeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArg 241
DB      580 CTCGATGCTGCTTTGTCGATGCTGTTTCAAGTTTCAAGTTGATATTCAGCCGTTTCA 639
  
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QY      242 AspMetIleGluGlyMetArgMetAspLeuTrpValSerArgTrpLeuThrPheAspGlu 261
DB      640 GATATGATCGAAGAAATCGATATGATCTTGAGGAAGTGCAGATATCAGAACTTTATGAG 699
QY      262 LeuTyrLeuTyrCysTyrTrpValAlaGlyThrValGlyLeuMetSerValProValMet 281
DB      700 CTATACCTATATGTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 759
QY      282 GlyIleAlaProGluSerLeuValSerThrGluSerValTyrAsnAlaAlaLeuAlaLeu 301
DB      760 GGCATGCACTGAAATCAAGGCAACACAGAGATGTATATATATATATATATATATATAT 819
QY      302 GlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGly 321
DB      820 GGTATCGGAAATCAACTATCAACACTTCTCAGAGATGTCGAGAAATGCCAGAAAGAGA 879
QY      322 ArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePhe 341
DB      880 AGAGCTCACTTAACCTCAAGATGAATTAACACAGGAGGCTCTCCGACGATGACATATTT 939
QY      342 AlaGlyArgValThrAspValTrpArgAsnPheMetLeuGlyGlnIleGlnArgAlaArg 361
DB      940 ACTGGAAGAGTACTGATTAATGAGAGAGCTTTATGAAAGACATTCAGAGGCAAGA 999
QY      362 LysPhePheAspGluSerGlyLeuGlyValThrGluLeuAspSerAlaSerArgTrpPro 381
DB      1000 AAGTTCTTCATGAGGCGAGAGAGAGAGAGTACACACTGAGCTCACTGACGATGGCT 1059
QY      382 ValLeuThrAlaLeuLeuLeuTyrArgGlyIleLeuAspGluIleGluAlaAsnAspTyr 401
DB      1060 GTATCGGAGCATCTTGCTGCTGTGACCGCAATATCTGACGAGATGAGAGCCATGATC 1119
QY      402 AsnAsnPheThrArgArgAlaTyrValSerIleProGlyValLeuLeuThrLeuProIle 421
DB      1120 AACCACTTCACAAAGAGAGCTTATGTGAGCAAAATCAAGAAAGCTTATTCCTTACCTAT 1179
QY      422 AlaTyrAlaLysSerLeuValProProAsnArgThr 433
DB      1180 GCTTATGCAAAATCTCTGTGTGCCCCCTTACAGAACT 1215
  
```

RESULT 5

US-09-180-342-2
 Sequence 2, Application US/09180342A
 Patent No. 6239331

GENERAL INFORMATION:
 APPLICANT: Drake, Caroline R.

APPLICANT: Bird, Colin R.

APPLICANT: Schuch, Wolfgang W.

TITLE OF INVENTION: Enhancement of Gene Expression

FILE REFERENCE: SE850156

CURRENT APPLICATION NUMBER: US/09/180,342A

CURRENT FILING DATE: 1998-11-05

EARLIER APPLICATION NUMBER: PCT/GB97/01414

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: UK 9611981.3

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 1239

TYPE: DNA

ORGANISM: Lycopersicon esculentum

US-09-180-342-2

Alignment Scores:

Pred. No.:	1.44e-195	Length:	1239
Score:	1750.00	Matches:	344
Percent Similarity:	86.84%	Conservative:	32
Best Local Similarity:	79.45%	Mismatches:	33
Query Match:	77.09%	Indels:	24
DB:	3	Gaps:	3

QY 103 SerGluLysValLysPheValValLeuLysGlnAlaLeuValLysArgGlnLeu 122
 DB 229 AGGAGCAATGGTGTACGACGCTGTAATCTCGTAAGCTGCACTAATGTAACCTGATTA 288
 QY 123 ArgSerThrAspAspLeuGluValLysProAspIleValValProGlySerLeuGlyLeu 142
 DB 289 CGTAGTACTACCAACTGAGGTAAACCGACATTCACATCTGAAACCTTGACATT 348
 QY 143 LeuSerGluAlaLysPheValLysPheValLysGlyValLysGlyValLysGlyValLys 162
 DB 349 CTTTCGAGGCTTACGACGATGCGAGAGGTTTGGCGAATAACCTTAACCTTCAAT 408
 QY 163 LeuGlyThrLysLeuMetThrProGluArgArgAlaIleThrAlaIleThrValLys 182
 DB 409 TTGGGTACCATGTGTATGACACCAAGGCGCTGCAATATGAGGCTATTACGTTGG 468
 QY 183 CysArgArgThrAspLeuLeuValLysGlyValLysGlyValLysGlyValLysGlyVal 202
 DB 469 TGTAGGCGTACTGACGACGATGAGACGACCTTAATGCTAATGTAACACCCGCTGCT 528
 QY 203 LeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeu 222
 DB 529 CTTGACAGATGGAGAACCGTTTGGAGAGCTGTTTAACGCGACCTTTCGATATGTTG 588
 QY 223 AspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAsp 242
 DB 589 GACGAGACCTTAGTACACTGTGACCAATTTCCGTGGACATCCACTTTTGGGAC 648
 QY 243 MetIleGluGlyMetArgMetAspLeuTrpLysSerArgTrpLysThrPheAspGluLeu 262
 DB 649 ATGATCGAGGCGATGAGAAATGATCTTCGTAACTCTCTTATTAAGAAATTTTGATGATTG 708
 QY 263 TyrLeuLysCysTrpTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282
 DB 709 TATTTGTACTCTACTACTGCTGAGAGAACCGTGGCTTATGTCAGTGGCTTATCAGGGA 768
 QY 283 IleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGly 302
 DB 769 ATTGCACGAGAGTAAGCTACTGATCTGTTTACACCGCACACAGCATTAAGT 828
 QY 303 LeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArg 322
 DB 829 ATAGCTAACCAAGCTTAAATAATCTTGAAGAGACGCTGGAGAGACCACTGAGGCTCGT 888
 QY 323 ValTyrLeuProGluAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAla 342
 DB 889 GGTATCTCTCCACAGAGACGCTGCTCAAGCTGGAATGAGTACAGAGACATTTTCGCA 948
 QY 343 GlyArgValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaArgLys 362
 DB 949 GGTCTGTACAGACAGAGTGGAGGATTTTCATGAAAAAGCATTCACCGTCTCGTAA 1008
 QY 363 PhePheAspGluSerGlyLysGlyValThrGluLeuAspSerAlaSerArgTrpProVal 382
 DB 1009 TTTTTCGACGAACTGAAAAAGGAGTTCAGACTTTCTAGTCAATCAAGTTCAGATT 1068
 QY 383 LeuThrAlaLeuLeuLeuLysArgLysIleLeuAspGlnIleGlnAlaAsnAspLysArg 402
 DB 1069 TGGGCGACCTGTGTCTATAGAAAGATTTCGAGCAAAATCGAGGCTAACGATTTAAT 1128
 QY 403 AsnPheThrArgArgAlaLysValSerLysProLysLeuLeuThrLeuProIleAla 422
 DB 1129 AATTTTACTTAACGTCCTTACGTTTCTTAAGAGCAAAAACTTATTCGCTCTTCCATCGCT 1188
 QY 423 TyrAlaLysSerLeuValProProAsnArgThrSerSer 435
 DB 1189 TAGGTAAGAGCTGGTTCACCACTAAGACAGCTAGC 1227
 RESULT 7
 US-07-995-950-2
 ; Sequence 2, Application US/07995950
 ; Patent No. 5304478
 ; GENERAL INFORMATION:

; APPLICANT: Bird, Colin R.
 ; APPLICANT: Grierson, Donald
 ; APPLICANT: Schuch, Wolfgang W.
 ; TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS
 ; TITLE OF INVENTION: DERIVED THEREFROM
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cushman, Darby & Cushman
 ; STREET: 1615 L Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20036-5601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/995,950
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/625,664
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kokulis, Paul N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: PNK/3893/82895/MCW
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-861-3000
 ; TELEFAX: 202-822-0944
 ; TELEX: 248453 cush
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1646 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-07-995-950-2
 Alignment Scores:
 Pred. No.: 2,94e-193 Length: 1646
 Score: 1732.00 Matches: 346
 Percent Similarity: 85.68% Conservative: 31
 Best Local Similarity: 78.64% Mismatches: 36
 Query Match: 76.30% Indels: 27
 DB: 1 Gaps: 4
 US-09-847-081B-2 (1-440) x US-07-995-950-2 (1-1646)
 QY 1 MetSerMetSerValAlaLeuLeuTrpValLysSerProThrSerGluValSerAsnGly 20
 DB 195 CTCAGATCTCTGTTGCTGTTATGGGTTGTTCTCC---TGAGCTCTCAAAATGG 251
 QY 21 ThrGlyLeuLeuAspSerValArgGlyLysAsnArgValPheValSerSerArgPheLeu 40
 DB 252 ACAAGTTTCATCAAGTCACTCCGAGAGGGAACCGTTTTTTTGATTCAATCG----- 302
 QY 41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgGlyLysGlyValLysGlyValLysGlyVal 60
 DB 303 ---AGCATAGAAATTTGTGTGTCATAGAGAAATCAATAGAGCT----- 344
 QY 61 AsnPheGlySerLeuIleAlaAspProArgTrpSerCysLeuGlyGlySerArgThrGlu 80
 DB 345 -----GATCGAAGCAAACTAAT 362
 QY 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyLysMetThr 100
 DB 363 AATGACGCAAAATTTTCTGTACGCTGCTATATTTGGCTACTCCATCTGGAGAACGAGAG 422
 QY 101 ValSerSerGluLysLeuValTyrAspValValLeuLysGlnAlaAlaLeuValLysArg 120

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423 ATGACATCGGAACACATGCTATCATGCTTTGAGCGCAGCCCTGCTGAAGAG 482
121 GlnleuA9SerThrAspAspLeuGluValLysProAspIleValProGlyAsnLeu 140
483 CACTGAGATCTTCAACAGATTAGAGGAGGAGCGGATATCTTATTCGGGGAAATTG 542
141 GlyLeuLeuSerGluValATyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThr 160
543 GCGCTTGTTGAGTGAAGCATATGATAGGTGTGTGAAGTATGTGCGAGATATGCAAAAGCG 602
161 PheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTyrAlaIleTyr 180
603 TTTAACTTAGGAACTATGCTATGATGATCTCCGAGAGAAAGAGGCTATCTGGGCAATATAT 662
181 ValTyrCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrPro 200
663 GTATGTCACAGAAACAGATGATGATCTGTGATGCGCCAAAGCAATATATATATATATATAT 722
201 GlnAlaLeuAspArgTyrGluThrArgLeuGluAspIlePheSerGlyArgProPheAsp 220
723 GCAGCTTAGATAGGTGGGAAATAGCGCTAGAGAGATGTTTCAATGGCGCGCATTTGAC 782
221 MetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPhe 240
783 ATGCTCGATGGGCTTGTGTCGATACAGTTTCTAATCTTCCAGTATATTCAGCCATTC 842
241 ArgAspMetIleGluGlyMetArgMetAspLeuTyrPylsSerArgTyrLysThrPheAsp 260
843 AGAGATAGATGATGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 902
261 GluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProVal 280
903 GAACATACCTTATATGTTATATATGTTGCTGATGCTGATGCTGATGCTGATGCTGATGCT 962
281 MetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAla 300
963 ATGGGTATCGCCCGTGAATCAAGGCAACAGAGAGCGATATATATGCTGCTTGGCT 1022
301 LeuGlyLeuAlaAsnGluLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArg 320
1023 CTGGGATCGCAATCAATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1082
321 GlyArgValTyrLeuProGluAspGluLeuAlaGlyLeuSerAspGluAspIle 340
1083 GGAAGAGCTTACTTCTCCATGATGATATTAAGCAGCAGGCTTATCCGATGATGATATTA 1142
341 PheAlaGlyArgValThrAspLysTyrArgAsnPheMetLysLysGlnIleGlnArgAla 360
1143 TTTGCTGGAAGGATGACCGATTAATGAGAAATCTTATGAGAAACAAATACATAGGCGCA 1202
361 ArgLysPhePheAspGluSerGlyLysGlyValThrGluLeuAspSerLysSerArgTyr 380
1203 AGAAAGTCTTGTGAAGAGCAGAGAAAGCGGAGCAAGTGAAGCTCAGCTAGTATGATTC 1262
381 ProValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGlnAlaAsnAsp 400
1263 CTTGATGCGCATCTTGTGCTTGTGATCCGCAAAATCAATGATGATGATGATGATGATGAT 1322
401 TyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuPhe 420
1323 TACAACAACCTTCAACAAGAGAGCATATGATGAGCAAAATCAAGCAAGTATGATGATTC 1382
420 CilleAlaTyrAlaLysSerLeuValProProAsnArgThrSerSerProLeuAlaLys 439
1383 TATGCAATATGCAAAATCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1434

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RESULT 8
 US-08-300-582-2
 Sequence 2, Application US/08300582
 Patent No. 5750865
 GENERAL INFORMATION:
 APPLICANT: BIRD, COLIN R.

```

APPLICANT: GRIERSON, DONALD
TITLE OF INVENTION: SCHUCH, WOLFGANG W.
TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS
TITLE OF INVENTION: DERIVED THEREFROM
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,582
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,523
FILING DATE: 12-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 3893/95874
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-300-582-2
Alignment Scores:
Pred. No.: 2,94e-193 Length: 1646
Score: 1732.00 Matches: 346
Percent Similarity: 85.68% Conservative: 31
Best Local Similarity: 78.64% Mismatches: 36
Query Match: 76.30% Indels: 27
Gaps: 4
US-09-847-081B-2 (1-440) x US-08-300-582-2 (1-1646)
QY 1 MetSerMetSerValAlaLeuLeuTyrValValSerProThrSerGluValSerAsnGly 20
DB 195 CTCGAATGCTCTGTTGCTTGTATGAGGTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 251
QY 21 ThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu 40
DB 252 ACAAGTTTCAATGAAATAGTCGCGGAGGAAACCGTTTTTTATGATATCG----- 302
QY 41 AlaArgAspArgAsnLeuMetTyrAsnGlyArgIleLysLysGlyGlyArgGlnArgTyr 60
DB 303 ---AGCATAGGAATTTGGTGTCCAAATGAGAGAAATCAATAGAGGT----- 344
QY 61 AsnPheLysSerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGlu 80
DB 345 -----GGTGGAAAGCAAACTAAT 362
QY 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThr 100
DB 363 AATGACGGAATTTTCTGACGCTCTGCTATTTTGGCTACTCATCTGAGAGAGCGAGC 422
QY 101 ValSerSerGluLysLysValTyrAspValValLeuLysGlnAlaLeuValLysArg 120

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Db	423	ATGACATCGGAACAGATGGCTATCATGTGTTTTGAGCAGACGCCTTGGTGAAGAAG	482
OY	121	GlnLeuAsgSerThrAspAspLeuGluValIysProAspIleValAlaProGlyAsnLeu	140
Db	483	CACCTGAAATCTAACCAATGATTGAAGAAGCCGGATATCCATATTCGGGGAAATTTG	542
OY	141	GlyLeuLeuSerGlnAlaIleTyraAspArgCysGlyIleValCysAlaGluThyTrpAlaLysThr	160
Db	543	GGCTTTGTGAGTAAGAACATATATATAGTGTTGGTGAAGATATGTGCAGAGATATCAAAGAG	602
OY	161	PheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIleTyx	180
Db	603	TTTAACCTTAGGAACATATGCTATATGACTCCCGAGAGAAAGAGGCTATCTGGSCAATATAT	662
OY	161	ValITrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrPro	200
Db	663	GTATGGTGCAGAAAGAACAGATGAACCTGTGTGATGGCCCCAAAGCATCATATATATACC	722
OY	201	GlnAlaLeuAspArgITrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAsp	220
Db	723	GCAGCGCTTAGATAGGAGGGGAAATAGGCTAGAAAGATGTTTCAATAGGGGGCCATTGAGC	782
OY	221	MetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPhe	240
Db	783	ATGCTCGATGCGTCTTGTCCGATACAGTTTCTTACTTCCAGTTGATATATGACCATTC	842
OY	241	ArgAspMetIleGluGlyMetArgMetAspLeuITrpLysSerArgTyrllysThrPheAsp	260
Db	843	AGAGATATGATGTAAGGAATGGTATGGACTTGAGAAAATCGAGATVACAAAACTTCGAC	902
OY	261	GluLeuTyrlleuTyxCysEtyrTyValAlaGlyThyTrpValGlyLeuMetSerValProval	280
Db	903	GAACATAACCTTATATGTTATATATGTGCTGATGGTGGTATGATGATGATTCCAATT	962
OY	281	MetGlyIleAlaProGluSerLysAlaThrTrpGluSerValTyraAsnAlaAlaLeuAla	300
Db	963	ATGGGTATACGCCCTGGAATCAAAAGCACACAGAGCGTATATAAAGCTCTTGGCT	1022
OY	301	LeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyIleAspAlaArgArg	320
Db	1023	CTGGGGATCGCAATCAATTACTAACAATCTCAGAGATGTTGGAGAAGATGCCAGAAGA	1082
OY	321	GlyArgValTyrlleuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle	340
Db	1083	GGAAAGACTACTTCCTCCAAATGAATTATGACACAGCGCGCTATCCGATGAAGATATATA	1142
OY	341	PheAlaGlyArgValIThrAspLysITrpArgAsnPheMetLysIleGlnArgAla	360
Db	1143	TTTGCTGGAAGGGGTACCGATTAATGGAATCTTTATGAAGAAACAAATATCATATGCGCA	1202
OY	361	ArgLysPhePheAspGluSerGluLysGlyValIThrGluLeuAspSerAlaSerArgTrp	380
Db	1203	AGAAAGTCTTTGATGAGGACAGAAAGGCGTGAAGCAATGAGCTCAGCTAGTATGATTTC	1262
OY	381	ProValleuThrAlaLeuLeuLeuTyrlArgLysIleLeuAspGluIleGluAlaAsnAsp	400
Db	1263	CCTGATAGGCAATCTTGCTCTTGAACGCAAAATACAGATGAGATGGAACCAATGAC	1322
OY	401	TyrAsnAsnPheIThrArgArgAlaITyrAlaSerLysProLysLysLeuLeuIThrLeuPr	420
Db	1323	TACACAACTTCACAAAGAGACATATGTAGCAAAATCAAAACCAAGTTGATGATTCACC	1382
OY	420	oileAlaTyralylserLeuValProProAsnArgIThrSerSerProLeuAlalys	439
Db	1383	TATTGCATATGAAAATATCTTGTGCTCTCT-----ACAAAACGCGCTCTTTCAAA	1434

```

1  APPLICANT: Grill, Laurence K.
2  APPLICANT: Kumagai, Monto H.
3  APPLICANT: Della-Cioppa, Guy R.
4  TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
5  TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
6  NUMBER OF SEQUENCES: 19
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: Virginia C. Bennett
9  STREET: 1211 East Morehead Street, PO Drawer 34009
10 CITY: Charlotte
11 STATE: No. 5705624th Carolina
12 COUNTRY: USA
13 ZIP: 28234
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent in Release #1.0, Version #1.30
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/579,667
22 FILING DATE:
23 CLASSIFICATION: 435
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Bennett, Virginia C.
26 REGISTRATION NUMBER: 37,092
27 REFERENCE/DOCKET NUMBER: 627-196
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 919-420-2200
30 TELEFAX: 919-861-3175
31 INFORMATION FOR SEQ ID NO: 9:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 749 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37 MOLECULE TYPE: cDNA
38 US-08-579-667-9
39
40 Alignment Scores:
41 Pred. No.: 2.15e-42 Length: 749
42 Score: 442.00 Matches: 98
43 Percent Similarity: 73.83% Conservative: 12
44 Best Local Similarity: 65.77% Mismatches: 11
45 Query Match: 19.47% Indels: 28
46 DB: 1 Gaps: 4
47
48 US-09-847-081B-2 (1-440) x US-08-579-667-9 (1-749)
49
50 QY 3 MetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGlyThrGly 22
51 Db 382 ATGTCTGGTGGCTTGTATTATGGCTTTTACCT--TGTGAGCTCTCAATGAGACAGA 438
52
53 QY 23 LeuLeuAspSerValArgGluGlyLeuAsnArgValPheValSerSerArgPheLeuAlaArg 42
54 Db 439 TTCCTGATTCACGAAAGGAGGAAACCGGGTTTGTGCTGCTG-----AGG 486
55
56 QY 43 AspArgAsnLeuMetTrpAsnGlyValArgIleuValGlyValArgGlnArgTrpAsnPhe 62
57 Db 487 CARGAGATTTTACTGTGCATATGAGAGATCAAAAGAGCTGGAAACAAAGCTGAAATTTT 546
58
59 QY 63 GlySerLeuIleAlaAspProArgTrpGlySerCysLeuGlyGlySerArgThrGluLeuGly 82
60 Db 547 GGT----- 543
61
62 QY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMet---ThrVal 101
63 Db 550 -----TCCGTACGAGCTCTCGATGGTGGCTACACCAACGAGGAATGCGACACATG 600
64
65 QY 102 SerSerGluValuValTyAspValValLeuValGlnAlaLeuValTyAspGln 121
66 Db 601 ACATCAAGAACAGAGCTTATATATGTGTGATTGAACAACAGACGCTTATGTCMAAAGCCAG 666
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68 QY 122 LeuArgSerThrAspAspLeuGluValuValysProAspIleValValProGlyAsnLeuGly 141

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Db 661 CTGAGATCTACTGATGATTGAGAGTGAAGCGAGATCCCTCCCGGGAATTGAGC 720
Qy 142 LeuSerGluAlaTyrAspArgCys 150
Db 721 TTGTTAAGTGAAGCATATGATAGCTGT 747

RESULT 10
US-08-095-726-5
Sequence 5, Application US/08095726
Patent No. 5530189
GENERAL INFORMATION:
APPLICANT: Auslich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huel-Che B
TITLE OF INVENTION: Beta-Carotene Biosynthesis in
Genetically Engineered Hosts
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530189val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO. 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1198 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-095-726-5

Alignment Scores:
Pred. No.: 6.55e-33 Length: 1198
Score: 364.00 Matches: 95
Percent Similarity: 50.53% Conservative: 49
Best Local Similarity: 33.33% Mismatches: 124
Query Match: 16.04% Indels: 18
DB: 1 Gaps: 4

US-09-847-081b-2 (1-440) x US-08-095-726-5 (1-1198)

Qy 148 AsparGysGlyGluValCysAlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeu 167
Db 37 GACCAAGCAGACGACGACCATGCGCAAGGCTCGAAGATTGTCACACCGCTGCAAGCTG 96
Qy 168 MetThrProGluArgArgAlaIleTrrpAlaIleTrrpValTrrpCysArgArgThrAsp 187
Db 97 TTCGACCGCGGACCAACGCGTGAAGCGTGTGATGCTTACACCTGGTGGCGGACATGCAT 156
Qy 188 GluLeuValAspGlyProAsn-----AlaSerHisIleThr 199

Db 157 GACCTCATTCAGCAGACACCAAGCCCTGCGCCAGAGGCGCGGAGAGAGAGGCC 216
Qy 200 ProGlnAlaLeuAspArgTrrpGluThrArgLeuGlnAspIlePheSerGlyArgProPhe 219
Db 217 ACCGAGCGCTGGCGGCTGGCGGACCTGACCTGGCGGCGTTGAAGGGCCGAGATG 276
Qy 220 ---AspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGln 238
Db 277 CAGGATCCGGCTTCGCTGCTTCAGAGAGGTGGCGGTGACCCAGGATATAGCCCGCC 336
Qy 239 ProPheArgAspMetIleGluGlyMetArgMetAspLeuTrrpLysSerArgTrrpLysThr 258
Db 337 ATGGCGCTGCATCACCCTGACAGCGCTTGCATGACGTGACGTGCGACCCGATATGTCACC 396
Qy 259 PheAspGluLeuTrrpLysTrrpCysTrrpValAlaGlyThrValGlyLeuMetSerVal 278
Db 397 TTGAGGATACGCTGGCGCTGCTATCAGTGGCGGCGTGGTGGCTTGAATATGCGC 456
Qy 279 ProValMetGlyIleAlaProGluSerLysAlaThrArgLysSerValTyrAsnAla 298
Db 457 AGGGTATGGCGCTG-----CGGATGAGCGGTTGCTGATCGCGCC 498
Qy 299 LeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAla 318
Db 499 TGCATCTGGGCGTGGCGCTTCACAGCTGACGATATGCGCGGATATATTGACGATGCG 558
Qy 319 ArgArgGlyArgValTrrpLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGlu 338
Db 559 GCTATTGACCGCTGCTATCTGCGCGGAGGCTGACGATGCGGCGGCTGGCCCGAG 618
Qy 339 AspIlePheAla-GlyArgValThrAspLysTrrpArgAsnPheMetLysGlnIleGln 358
Db 619 AACATACCGCGCGGAGAAATCGCGCGCGCTGGCGCGG-TGG---CGAGGCTTATGCA 674
Qy 358 nArgAlaArgLysPheAspGluSerGlyLysGlyValThrGluLeuAspSerAlaSer 378
Db 675 TGCCGACAGCGGCTACATCTCTCCACGCGGCGGCTACACATCTGCGCGCGCTC 734
Qy 378 TrgTrrpProValLeuThrAlaLeuLeuLeuTrrpArgLysIleLeuAspGlnIleGln 398
Db 735 CGCGTGGCGGATCGCACCGCGCGGACGCTTACCGGAGATCGTAAAGTAAAGC 794
Qy 398 AsnAspTrrpAsnAsnPheThrArgArgAlaTrrpValSerLysProLysLysLeuLeu 418
Db 795 GCGCGAGGACGACCGCTGGATCGCCCGACACACGAAAGCTGAATAATTCGCAT 854
Qy 418 TrLeuProIleAla 422
Db 855 GCTGATGCGGCA 867

RESULT 11
US-08-096-043-5
Sequence 5, Application US/08096043
Patent No. 5530189
GENERAL INFORMATION:
APPLICANT: Auslich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huel-Che B
TITLE OF INVENTION: Lycopen Biosynthesis in
Genetically Engineered Hosts
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:

Best Local Similarity: 33.33% Mismatches: 124
 Query Match: 16.04% Indels: 18
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 168 MetThrProGluArgArgAlaIleThrAlaIleTyrValTyrPheArgArgThrAsp 187
 97 TTCGACCCGCGCACCGCCGCTGAGCGTCTGATCTACCTGCTGCGCCACTGCGCAT 156
 188 GluLeuValAspGlyProAsn-----AlaSerHisIleThr 199
 157 GACGTCATTTGACGACCAACCAACCGCTTCCGACGAGCCGCGGAGAGAGAGAGCC 216
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 259 PheAspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerVal 278
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 279 ProValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaIle 298
 457 AGGGGATGGCGGTG-----CGGATGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 498
 299 LeuAlaLeuGlyIleValAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAla 318
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 319 ArgArgGlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGlu 338
 559 GCTATTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 618
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 735 GCGCGGGCGGATCGCACCGCGCGGAGGTCTACCGGAGATCGGTATTAAAGTAAAGC 794
 398 AsnAspTyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuTh 418
 795 GCGCGGAGCGCGCGCTGGATCGCGCGACACACGACCAAGGTAAGGTAAGGTCAT 854
 418 rLeuProIleAla 422
 855 GCTGATGCGCGCA 867

APPLICANT: Mukharji, Indrani
 APPLICANT: Proffitt, John H.
 APPLICANT: Yarger, James G.
 APPLICANT: Yen, Hwei-Che B.
 TITLE OF INVENTION: Biosynthesis of Zeaxanthin and
 TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Welsh & Katz, Ltd.
 STREET: 120 S. Riverside Plaza, 22nd Floor
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/096,623A
 FILING DATE: 22-JUL-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/805,061
 FILING DATE: 09-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/662,921
 FILING DATE: 28-FEB-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/562,674
 FILING DATE: 03-AUG-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/525,551
 FILING DATE: 18-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/487,613
 FILING DATE: 02-MAR-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Gamson, Edward P.
 REGISTRATION NUMBER: 29,381
 REFERENCE/DOCKET NUMBER: AMO-006.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 655-1500
 TELEFAX: (312) 655-1501
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1198 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 POSITION IN GENOME:
 MAP POSITION: -15 to 1183
 UNITS: bp
 US-08-096-623A-5

Alignment Scores:
 Pred. No.: 6.55e-33 Length: 1198
 Score: 364.00 Matches: 95
 Percent Similarity: 50.53% Conservative: 49
 Best Local Similarity: 33.33% Mismatches: 124
 Query Match: 16.04% Indels: 18
 DB: 1 Gaps: 4
 US-09-847-081b-2 (1-440) x US-08-096-623A-5 (1-1198)

148 AspArgCysGlyValCysAlaGluThrAlaLeuThrPheTyrLeuGlyThrLysLeu 167
 37 GACCACGCCACGACGACCATGGCCCAACGGCTCGAAGATTGGCCACCGCTGCGAAGCTG 96
 168 MetThrProGluArgArgAlaIleThrAlaIleTyrValTyrPheArgArgThrAsp 187

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Qy      220 ---AspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGln 238
Db      277 CAGGATCCGCGCTTCTGCTTTCAGAGGAGTGGCGCGTACCCAGCGATTAAGCCCGCC 336
Qy      239 ProPheArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTrpLysThr 258
Db      337 ATGGCGCTCGATCACTCGACCGCTTGGGATGGAGCTGACGCTCAGACCCGGATGTGACC 396
Qy      259 PheAspGluLeuTyrlleuTyrlleuTyrlleuValAlaGlyThrValGlyLeuMetSerVal 278
Db      397 TTTGAGGATACGCTGCTACTGCTATCAGTGGCGGCGGTGGTGTGATGATGGCC 456
Qy      279 ProValMetGlyIleAlaProGluSerLysAlaIleThrGluSerValTyrlleuAlaIle 298
Db      457 AGGGTATGGGCGGTG-----CGGATGAGCGGCTGCTGATCGCGCC 498
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Db      499 TCCGATCTGGGCTGGCTTCCAGCTGACGAAATATGGCCGGGAAATTTTGAACGATGGC 558
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Qy      339 AspIlePheAla-GlyArgValThrAspLysTrpArgAsnPheMetLysLysGlnIleGln 358
Db      619 AACTATGCCCGCGGAGATGCCCGCGCTGGCGCGG-TGG--CGAGGCTTATTGA 674
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Db      675 TCCCGCAGGCGCTACTATCTCTCCAGCGCGGCTACACGATCTCGCGCGCGCTC 734
Qy      378 IArgTrpProValLeuThrAlaLeuLeuLeuTyrlleuValAspIleGlnIle 398
Db      735 CGCGTGGGCGATCGCACCGCGCGAGCTTACCGGAGATCGGATTAAGTAAAGC 794
Qy      398 aAsnAspTyrlleuAsnAsnPheThrArgArgAlaTyrlleuSerLysProLysLysLeuLeuTh 418
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; ZIP: 60563-8437
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,004A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 561898val B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7087172447
; TELEFAX: 7087172430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1083 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-331-004A-1
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Alignment Scores:
Pred. No.: 1,096-32 Length: 1083
Score: 361.50 Matches: 95
Percent Similarity: 50.18% Conservative: 48
Best Local Similarity: 33.33% Mismatches: 126
Query Match: 15.93% Indels: 17
DB: 1 Gaps: 3
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US-09-847-081B-2 (1-440) x US-08-331-004A-1 (1-1083)
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Db      24 GACCAAGCGCAGCAGACGATGCTGCTGATGCTCTACACCTGATGCGGCGACATG 83
Qy      168 MetThrProGlnArgArgAlaIleThrAlaIleTyrlleuValThrCysArgArgThrAsp 187
Db      84 TTCGACCCGGCCACCGCGGCTGATGCTGATGCTCTACACCTGATGCGGCGACATG 143
Qy      188 GluLeuValAspGlyProAsn-----AlaSerHisIleThr 199
Db      144 GACGCATTTGAGACGACCAAGCCAGCTTCCGACGAGCGCGCGGAGAGAGAGGCC 203
Qy      200 ProGlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPhe 219
Db      204 ACCCAGCGCTGGCGCGCTGCGCACGCTGACCTGGCGCGGCTTGAAGGCGCGAGATG 263
Qy      220 ---AspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGln 238
Db      264 CAGGATCCGCGCTTCTGCTTTCAGAGGAGTGGCGCTGACCCAGCGATTAAGCCCGCC 323
Qy      239 ProPheArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTrpLysThr 258
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Qy      259 PheAspGluLeuTyrlleuTyrlleuTyrlleuValAlaGlyThrValGlyLeuMetSerVal 278
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Qy      279 ProValMetGlyIleAlaProGluSerLysAlaIleThrGluSerValTyrlleuAlaIle 298
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Qy      299 LeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyLysAlaIle 318
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 Qy 378 rArgTrpProValleuThrAlaleuLeuLeuTyrrArglyslleuaspGlnileg1 398
 Db 725 CGCCTGGCGCATCGCCACCGCCCGCAGCGCTCTACCGGAGATCGGTATTAAAGTAAAGC 784
 Qy 398 aAsnAspTyrrAsnAsnphethrArghArAlaTyrrValSerlyspProlyslsLeuLeuth 418
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 Qy 418 rLeuProileAla 422
 Db 845 GCTGATGCGGCA 857

RESULT 15

PCT-US95-13937A-1
 : Sequence 1, Application PC/TUS9513937A
 : GENERAL INFORMATION:
 : APPLICANT: Hauptmann, Randal
 : APPLICANT: Eschenfeldt, William H
 : APPLICANT: English, Jami
 : APPLICANT: Brinkhaus, Friedhelm L
 : TITLE OF INVENTION: Enhanced Carotenoid Accumulation
 : TITLE OF INVENTION: In Storage Organs of Genetically
 : NUMBER OF SEQUENCES: 9
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Amoco Corporation, Law Dept
 : STREET: 55 Shuman Boulevard, Suite 600
 : CITY: Naperville
 : STATE: IL
 : COUNTRY: USA
 : ZIP: 60563-8437
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.24
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US95/13937A
 : FILING DATE:
 : CLASSIFICATION:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Galloway, Norval B
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 7087172447
 : TELEFAX: 7087172430
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1083 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : PCT-US95-13937A-1

Alignment Scores:

Pred. No.: 1.09e-32 Length: 1083
 Score: 361.50 Matches: 95
 Percent Similarity: 50.18% Conservative: 48
 Best Local Similarity: 33.33% Mismatches: 126
 Query Match: 15.93% Indels: 17
 DB: 5 Gaps: 3

US-09-847-081B-2 (1-440) x PCT-US95-13937A-1 (1-1083)

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 Db 24 GACCACGCCACGACGACACATAGCCCAACGCGCTCGAAAAGTTTCCACCGCTGGCAAGCT 83
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 Qy 239 ProPheArgAspMetIleGluGlyMetArgMetAspLeuTrrPylsSerArgTyrrLysThr 258
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 Qy 279 ProValMetGlyIleAlaProGluSerLysAlaThrThrLysSerValTyrrAsnAla 298
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 Qy 299 LeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAla 318
 Db 486 TGGCATTTGGGGCTGGCTTCCAGCTGACGATATGCCCGGATATTATTAGAGATGCG 545
 Qy 319 ArgArgGlyArgValTyrlleuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGlu 338
 Db 546 GCTATTGACCGCTACTCTGCGCGCGAGTGGCTGAGAGATCGCGGCTGACCCCGAG 605
 Qy 339 Aspllepheala-glyarvalthrAsplystrArghAnphemetlyslsGlnileg1 358
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 Qy 378 rArgTrpProValleuThrAlaleuLeuLeuTyrrArglyslleuaspGlnileg1 398
 Db 725 CGCCTGGCGCATCGCCACCGCCCGCAGCGCTCTACCGGAGATCGGTATTAAAGTAAAGC 784
 Qy 398 aAsnAspTyrrAsnAsnphethrArghArAlaTyrrValSerlyspProlyslsLeuLeuth 418
 Db 785 GCGCGAGGAGCAGCGCTGTGATCGCGCCAGACACGCAAGAGTGAATAATTTGCCAT 844
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 Db 845 GCTGATGCGGCA 857

Search completed: January 16, 2004, 08:48:56
 Job time : 104 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 16, 2004, 08:00:33 ; Search time 444 Seconds
(without alignments)
3493.009 Million cell updates/sec

Title: US-09-847-081B-2

Perfect score: 2270
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1737	76.5	1239	9	US-09-371-307-75	Sequence 75, Appli
4	1737	76.5	1239	12	US-10-401-321-75	Sequence 75, Appli
5	1542	67.9	1269	10	US-09-938-842A-729	Sequence 729, App
6	468	20.6	684	13	US-10-149-759-53	Sequence 53, Appli
7	372	16.4	1026	15	US-10-156-761-1013	Sequence 1013, Ap
8	372	16.4	9025608	15	US-10-156-761-1	Sequence 1, Appli
9	368	16.2	948	15	US-10-156-761-1642	Sequence 1642, Ap
10	368	16.2	9025608	15	US-10-156-761-1	Sequence 1, Appli
11	359.5	15.8	945	13	US-10-128-713A-15	Sequence 15, Appli
12	350.5	15.4	1232	14	US-10-041-472-1	Sequence 1, Appli
13	336.5	14.8	891	11	US-09-941-947A-33	Sequence 33, Appli
14	336.5	14.8	891	13	US-10-218-118-9	Sequence 9, Appli
15	327.5	14.4	1008	15	US-10-166-037-4	Sequence 4, Appli
16	326	14.4	8625	11	US-09-920-923-1	Sequence 1, Appli
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18	324	14.3	908	10	US-09-547-267-4	Sequence 4, Appli
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21	306	13.5	7252	11	US-09-918-740-75	Sequence 75, Appli
22	293	12.9	536165	11	US-09-939-964-1	Sequence 1, Appli
23	273.5	12.0	2174	8	US-08-781-986A-202	Sequence 202, App
24	272.5	12.0	864	13	US-10-358-917-9	Sequence 9, Appli
25	230	10.1	3807	12	US-10-438-784-2	Sequence 2, Appli
26	230	10.1	5898	12	US-10-438-784-1	Sequence 1, Appli
27	221	9.7	825	12	US-10-438-784-6	Sequence 6, Appli
28	204	9.0	912	10	US-09-738-626-595	Sequence 695, App
29	204	9.0	3309400	10	US-09-738-626-1	Sequence 1, Appli
30	198	8.7	876	10	US-09-738-626-2673	Sequence 2673, Ap
31	197.5	8.7	900	15	US-10-156-761-1643	Sequence 1643, Ap
32	170	7.5	405	13	US-10-259-678-345	Sequence 345, App
33	167.5	7.4	1092	13	US-10-358-917-1	Sequence 1, Appli
34	161	7.1	1173	12	US-10-359-493-42261	Sequence 42261, A
35	145.5	6.4	408	15	US-10-166-037-8	Sequence 8, Appli
36	141	6.2	1347	13	US-10-032-585-6355	Sequence 6355, Ap
37	139.5	6.1	1335	12	US-10-359-493-45750	Sequence 45750, A
38	138.5	6.1	1587	15	US-10-128-714-7505	Sequence 7505, Ap
39	135.5	6.0	1563	15	US-10-128-714-2505	Sequence 2505, Ap
40	135.5	6.0	1565	15	US-10-128-714-1505	Sequence 1505, Ap
41	135.5	6.0	1730	15	US-10-128-714-5505	Sequence 5505, Ap
42	135.5	6.0	3665	15	US-10-128-714-5505	Sequence 5505, Ap
43	135.5	6.0	3730	15	US-10-128-714-5505	Sequence 5505, Ap
44	126	5.6	2097	13	US-10-240-965-172	Sequence 172, App
45	123	5.4	984	15	US-10-156-761-3904	Sequence 3904, Ap

ALIGNMENTS

RESULT 1
US-09-847-081B-1
Sequence 1, Application US/09847081B
Patent No. US20020128464A1
GENERAL INFORMATION:
APPLICANT: BAYER AG
TITLE OF INVENTION: DNA encoding the tobacco phytoene synthase
FILE REFERENCE: Le A 34 326
CURRENT APPLICATION NUMBER: US/09/847,081B
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1728
TYPE: DNA
ORGANISM: Nicotiana tabacum
FEATURE:
NAME/KEY: CDS
LOCATION: (244)..(1566)
US-09-847-081B-1
Alignment Scores: 1.17e-274 Length: 1728
Pred. No.: 2270.00 Matches: 440
Score:

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 10
 Gaps: 0

US-09-847-081B-2 (1-440) x US-09-847-081B-1 (1-1728)

QY 1 MetSerMetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGly 20
 Db 244 ATGAGCAGTCTGTTGCTTTGTGGGTGTGTTTCCACCTCCGAGGTCTCGAATGG 303
 QY 21 ThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeu 40
 Db 304 ACAGGATGTTGGATTGAGTCCGAGAGAGAAACCCGCTTTGTATCATCCAGGTTCTTA 363
 QY 41 AlaArgAspArgAsnLeuMetTrpAsnGlyArgGlyLeuValArgGlyValArgGly 60
 Db 364 GCTCGAGATGAGAAATTTATGTGATGGATGGAGAAATCAAGAAAGTGGAGACAAAGTGG 423
 QY 61 AsnPheGlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGlu 80
 Db 424 AATTGGCTCTTATTTGCTGATCCAGATTTTCATCTTGGGTGATCAAGAACTGAA 483
 QY 81 LysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThr 100
 Db 484 AAGGGAACACCTTCTCTGTACAGTCCAGTTGGTGGCTAGCCGAGTGGAGAAATGACT 543
 QY 101 ValSerSerGlyValValValValValValValValValValValValValValVal 120
 Db 544 GTGTCATCAGAGAAAGAGTGTATGATGTGATTTAAAGCGGCGCTTGTAGTGAAGG 603
 QY 121 GlnLeuArgSerThrAspAspLeuGluValLysProAspIleValProGlyAsnLeu 140
 Db 604 CAGCTGAGATCTTACGATGATTTAGAGTGAAGCCGATTTGTTTCCAGGGAATTTG 663
 QY 141 GlyLeuLeuSerGluAlaIleAspArgCysGlyGlyValCysAlaGlyValAlaLysThr 160
 Db 664 GCGTTGTTGAGTGAAGCATATGATCGTTGGCGAAGATGAGCATATGAGCAAGACA 723
 QY 161 PheTyrLeuGlyThrIleLeuMetThrProGluValGlyGlyAlaIleTrpAlaIleTyr 180
 Db 724 TTTTACTTAGGAAACCAAGCTATATGACCCAGAGAAAGAGCATATGTGGCAATATAT 783
 QY 181 ValTrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrPro 200
 Db 784 GTGTGTCAGAGAGAACCGATGAGCTTGTGATGCGCTTAATGCATCCACATTAATCTCG 843
 QY 201 GlnAlaLeuAspArgTrpGluThrArgLeuGluValAspIlePheSerGlyArgProPheAsp 220
 Db 844 CAAGCTTATAGATAGGTGGAGACCAAGCTGGAGAAATTTTCAAGTGGCGGCATTTGAT 903
 QY 221 MetLeuAspAlaAlaLeuSerThrPheValSerArgPheProValAspIleGlnProPhe 240
 Db 904 ATGCTTATGATGCTCTTATTCGATCTGTCTCCAAATTTCTGTGATATTCAGCCATTC 963
 QY 241 ArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrIleThrPheAsp 260
 Db 964 AGAGATATGATTTGAGAGATGGATGGATGCTGTGAAATCCAGTTACAAACCTTTCAT 1023
 QY 261 GluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProVal 280
 Db 1024 GAGCATATCTCTATTTGTTACATATGTTCTGCTATCTAGAGATTGATAGAGTTCACATT 1083
 QY 281 MetGlyIleAlaProGluSerIleValThrThrGluSerValTyrAsnAlaAlaLeuAla 300
 Db 1084 ATGGATATTTGACCTCGAATCAAGGCAACACAGAGAGTATATATTAATGCTGCTTGGCT 1143
 QY 301 LeuGlyLeuAlaAsnGlyLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArg 320
 Db 1144 TTAGGCTTGGCAATCACTAACCAATATCTCAAGAGTGAAGAGATGCCAAGAA 1203
 QY 321 GlyArgValTyrLeuProGlnAspGluLeuValAlaGlyLeuSerAspGluAspIle 340

Db 1204 GGAAGATATCTTGGCTCAAGATGAATTAGACAGGCGAGGCTCTCCAGCAAGACATA 1263
 QY 341 PheAlaGlyArgValThrAspLysTrpArgAsnPheMetLysIleGlnIleArgAla 360
 Db 1264 TTGCTGGAAGAGTGAATGATTAAGTGGAGAACTTTATGAAAGAAATTCAGAGGGCG 1323
 QY 361 ArgLysPhePheAspGluSerGluValValThrGluLeuAspSerAlaSerArgTrp 380
 Db 1324 AGAAATTTCTTTGATGATGATGAGAGAAAGTGTCAAGAACTGAGCTGTGATGATGAG 1383
 QY 381 ProValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAsp 400
 Db 1384 CCGTGTAAACAGCGCTGCTGTGTATGCGCAAGATATTTGACAGATTTGAAGCCAAAGC 1443
 QY 401 TyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuPro 420
 Db 1444 TACACAACTTTCACAGAGAGGCTTATGTATAGCAAGCCAAAGAACTTTCACCTTCCC 1503
 QY 421 IleAlaTyrAlaLysSerLeuValProProAsnArgThrSerSerProLeuAlaLysThr 440
 Db 1504 ATTGCTATGCAAAATCTTGTGCCCCCTAATATGAACTTCTCTCCATGCAAGAAACA 1563

RESULT 2

US-09-847-081B-3
 ; Sequence 3, Application US/09847081B
 ; Patent NO. US20020128464A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BAYER AG
 ; TITLE OF INVENTION: DNA encoding the tobacco phytoene synthase
 ; FILE REFERENCE: Le A 34 326
 ; CURRENT APPLICATION NUMBER: US/09/847,081B
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 1712
 ; TYPE: DNA
 ; ORGANISM: Nicotiana tabacum
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (333)..(1565)
 ; NAME/KEY: unsure
 ; LOCATION: 135..139
 ; OTHER INFORMATION: Xaa is unknown or other
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: 51
 ; OTHER INFORMATION: n can be any nucleotide
 US-09-847-081B-3

Alignment Scores:

Pred. No.: 1.04e-215 Length: 1712
 Score: 1801.00 Matches: 357
 Percent Similarity: 87.93% Conservative: 29
 Best Local Similarity: 81.32% Mismatches: 24
 Query Match: 79.34% Indels: 29
 DB: 10 Gaps: 4

US-09-847-081B-2 (1-440) x US-09-847-081B-3 (1-1712)

QY 3 MetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGlyThrGly 22
 Db 333 ATGCTGTGCTCTGTTATGAGGTGTTTCACT--TGTGAAGTCTCAATATGGACAGCA 389
 QY 23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42
 Db 390 TTCTTGATTTCAAGTCGGGAGGGGAAACCGGTTTATTCGTCG-----AGG 437
 QY 43 AspArgAsnLeuMetTrpAsnGlyArgIleLysGlyGlyValArgGlnAlaGlyTrpAsnPhe 62
 Db 438 CATAGGATTTAGTGTCAATGAGAGAAACAGAGAGGTGTGAAACAAAGGTGAATTTT 497

QY 63 GlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluLysGly 82
 Db 498 GGT----- 500
 QY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMet---ThrVal 101
 Db 501 -----TCGTAAAGGCTGCTCTATGGTGGCTACACGGCGGAGAAATGGCGACGATG 551
 QY 102 SerSerGluLysValTyrAspValValLeuLysGlnAlaAlaLeuValLysArgGln 121
 Db 552 ACATCAGAAACAGATGCTTATGATGTGGTTTAAACAAGACGCTTTGATGAGAGGCGAG 611
 QY 122 LeuArgSerThrAspAspLeuGluValLysProAspIleValValProGlyAsnLeuGly 141
 Db 612 TTGAATCTGCTGATGATTTAGAGTGAAGCGGAGATCCCTCCCGGGAATTTGAGC 671
 QY 142 LeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPhe 161
 Db 672 TTGTGAGTGAAGCATATGATGTGAGTGAAGTATGACAGATATGCAAGACATTT 731
 QY 162 TyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTyrAlaIleTyrVal 181
 Db 732 TACTTGGGAACCATGTATATGATCTCCAGAGAGAGAGAGGCTATTTGGCAATATATGTG 791
 QY 182 TrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGln 201
 Db 792 TGTGTCAGAGAAACAGATGACCTTGTGATGCGCCAAAGCATCATATTAACCCCA 851
 QY 202 AlaLeuAspArgTrpGluThrArgLeuGluValAspIlePheSerGlyArgProPheAspMet 221
 Db 852 GCCTTAGATGAGGTGGAAAGACCGGCTTGAAAGTGTTCAGGGCGACCATTTGATATG 911
 QY 222 LeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArg 241
 Db 912 CTCGATGCTGCTTCTTCGATCTGTTCCAGATTTCAGTGAATTCAGCCGTTCCAGA 971
 QY 242 AspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGlu 261
 Db 972 GATATGATTTGAAGAGATGGATGACCTTGAGAGAGTCAGAGATATAGAACTTATGATG 1031
 QY 262 LeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMet 281
 Db 1032 CTTTACCTCTATGTTATTAACGTCCTGCTGATGAGTGGTGTGATGATGATTCATTTATG 1091
 QY 282 GlyIleAlaProGluSerLysValaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeu 301
 Db 1092 GGTATTTGCACTGATTTCAAAGCAACACAGAGCGATATATATGACCTTTGGCTTTA 1151
 QY 302 GlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGly 321
 Db 1152 GGAATCGCAATCACTAAGCAACATACCTCAGAGATGTTGAGAGATGCCAGAAAGAGA 1211
 QY 322 ArgValIleTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePhe 341
 Db 1212 AGAGCTCACTTAACCTCAAGATGAATTAAGACAGGAGGCTCTTTCGACATACATATTT 1271
 QY 342 AlaGlyArgValaThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaArg 361
 Db 1272 GCTGAAAAGTGAATGATGAGAGAGAGCTTTATGAGAGAGCAAAATCCAGAGGCGCAAGA 1331
 QY 362 LysPhePheAspGluSerGluLysGlyValaThrGluLeuAspSerAlaSerArgTrpPro 381
 Db 1332 AAGTCTTCGATGAGGACAGAGAGAGAGATTACACAACTAGCTCAGCTAGCAGATGGCT 1391
 QY 382 ValLeuThrAlaLeuLeuTyrArgLysIleLeuAspGlnIleGlnAlaAsnAspTyr 401
 Db 1392 GTATGGCATCTTCTGTTGACCGCCAAATATCGACGAGATGGAAGCCATATCATAC 1451
 QY 402 AsnAsnPheThrArgArgAlaTyrValaSerLysProLysLysLeuLeuThrLeuProIle 421
 Db 1452 AACCACTTCACAAAGAGCTTATGAGCAAAACCAAGAGAGCTTAATTTCCCTACTAT 1511
 QY 422 AlaTyrAlaLysSerLeuValProProAsnArgThr-SerSerProLeuAlaLys 439

Db 1512 GCTTATGCAAAATCTCTGTGCTGCCCTTACAGAACTTTGTACCTTAGCTAAG 1566
 RESULT 3
 US-09-371-307-75
 / Sequence 75, Application US/09371307A
 / Patent No. US20020053095A1
 / GENERAL INFORMATION:
 / APPLICANT: Brown, Sherri M.
 / APPLICANT: Heck, Gregory R.
 / APPLICANT: Piller, Kenneth J.
 / APPLICANT: Kishore, Ganesh M.
 / APPLICANT: Ellich, Ted D.
 / APPLICANT: Logusch, Eugene W.
 / APPLICANT: Rao, Sudabathula
 / APPLICANT: Ream, Joel E.
 / APPLICANT: Logusch, Sherry J.
 / TITLE OF INVENTION: Methods for controlling gibberellin levels
 / FILE REFERENCE: MOBT:216
 / CURRENT APPLICATION NUMBER: US/09/371,307A
 / CURRENT FILING DATE: 1999-08-10
 / NUMBER OF SEQ ID NOS: 89
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 75
 / LENGTH: 1239
 / TYPE: DNA
 / ORGANISM: Lycopersicon esculentum
 US-09-371-307-75
 Alignment Scores:
 Pred. No.: 7.02e-208 Length: 1239
 Score: 1737.00 Matches: 342
 Percent Similarity: 86.37% Conservative: 32
 Best Local Similarity: 78.98% Mismatches: 35
 Query Match: 76.52% Indels: 24
 DB: 9 Gaps: 3
 US-09-847-081b-2 (1-440) x US-09-371-307-75 (1-1239)
 QY 3 MetSerValAlaLeuLeuTyrValaLysSerProThrSerGluValaSerAsnGlyThrGly 22
 Db 1 ATGCTGTGGCTGTTATGAGGTGTTCTCTCT--TCGAGCTCTCAAAATGGGCAAGT 57
 QY 23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42
 Db 58 TTCATGATATAGTCGCGGAGGAAACCGTTTGTGATTATGCG-----AGG 105
 QY 43 AspArgAsnLeuMetTrpAsnGlyArgIleLysIleGlyArgGlnArgTrpAsnPhe 62
 Db 106 CATAGGAATTTGGTGTCCAAATGAGAGATCAATAGAGGT----- 144
 QY 63 GlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluLysGly 82
 Db 145 -----GGTGGAAAAGCAAACTAATTAATGGA 168
 QY 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSer 102
 Db 169 CGGAATTTTCTGTAACGCTGCTATTTTGGCTACTCATCTGGAGACGAGCATGCA 228
 QY 103 SerGluLysValaTyrAspValaLysLeuLysGlnAlaAlaLeuValaLysArgGlnLeu 122
 Db 229 TCGGAACAGAGGTCTATGATGTGTTTGAAGGACGAGCGCTGTGTAAGGCAATCG 288
 QY 123 ArgSerThrAspAspLeuGluValaLysProAspIleValValProGlyAsnLeuGlyLeu 142
 Db 289 AGATCTTACCAATGAGTTGAAGTGAAGCGGATATACCTAATTCGGGGAATTTGGGCTTG 348
 QY 143 LeuSerGluAlaTyrAspArgCysGlyGluValaCysAlaGluTyrAlaLysThrPheTyr 162
 Db 349 TTGAGTGAAGCATATGATGATGTGAGATATATGTCAGAGTATGCAAAAGACGTTTAC 408
 QY 163 LeuGlyThrLysLeuMetThrProGluArgArgAlaIleTyrAlaIleTyrValTrp 182

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Db      409 TTAGAACTATGCTAATGACTCCGAGAGAAAGGGCTATCTGGCAATATATATATG 468
Qy      183 CysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAla 202
Db      469 TGCAGAGAACAGATGAACCTTGTGATGGCCCAACGATCATATATATATATATATATAT 528
Qy      203 LeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeu 222
Db      529 CTAGATAGTGGGAAATAGGCTAGAGATGTTTTCATATGGGCGGCGCATTTGACATGCTC 588
Qy      223 AspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAsp 242
Db      589 GATGCTGCTTGTTCGATACAGTTTCTAATCTTCCAGTGTATATTCACCCATTCAGAAAT 648
Qy      243 MetIleGluGlyMetArgMetAspLeuTrpIlySerArgGlyArgIlyThrPheAspGluLeu 262
Db      649 ATGATTGAAGAAATCCGATATGACTTGGAAATTCGAAATCAAAAACCTTGACGAACTA 708
Qy      263 TyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282
Db      709 TACCTTATATGTTATATATGTTGCTGTACGGTGGGTTGATGAGTTCATATATATATG 768
Qy      283 IleAlaProGluSerIleValAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGly 302
Db      769 ATCCGCCCTGATCAAAAGCAACACAGAGCCGATATATATGCTGCTTGGCTCTGGGG 828
Qy      303 LeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyIleAspAlaArgGlyArg 322
Db      829 ATCCCAATTCATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 888
Qy      323 ValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAla 342
Db      889 GTCACTTGTGCTCAAGATGAATTAAGCACAGGAGGCTCATCGAATGAATATATATGCT 948
Qy      343 GlyArgValThrAspIlySerThrArgAsnMetIlySerGlnIleGlnArgAlaArgIly 362
Db      949 GGAAGGGGACCGATTAATGAAGATCTTTATGAAGAAACAAATCATATGAGGCAAGAAAG 1008
Qy      363 PhePheAspGluSerGluLeuGlyValThrGluLeuAspSerAlaSerArgTrpProVal 382
Db      1009 TTCTTGTATGAGCGAGCAATAGCGGTGACGAAATGACCTGACGATATATATATATAT 1068
Qy      383 LeuThrAlaLeuLeuLeuTyrArgIlyIleLeuAspGluIleGluAlaAsnAspTyrAsn 402
Db      1069 TGGGATCTTTGGTCTTGTACCGCAATTAATTAATTAATTAATTAATTAATTAATTAAT 1128
Qy      403 AsnPheThrArgArgAlaTyrValSerIlySerProIlyIleLeuThrLeuProIleAla 422
Db      1129 AACTTCAAAAGAGCATATGTGAGCAAAATCAAAAGATTGATTGCTATATGCA 1188
Qy      423 TyrAlaIlySerLeuValProProAsnArgTrpSerSer 435
Db      1189 TATGCAAAATCTCTGTGCTCTCAAAAACCTGCTCT 1227

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; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-10-401-321-75

Alignment Scores:
Pred. No.: 7,02e-208 length: 1239
Score: 1737.00 Matches: 342
Percent Similarity: 86.37% Conservative: 32
Best Local Similarity: 78.98% Mismatches: 35
Query Match: 76.52% Indels: 24
Gaps: 3

US-09-847-081b-2 (1-440) x US-10-401-321-75 (1-1239)

Qy      3 MetSerValAlaLeuLeuTrpValValSerProThrSerGluValSerAsnGlyThrGly 22
Db      1 ATGCTGTGCTGCTGTTATGAGTGTGTTCTCTCT---TGTGACGCTCAATATGGAACAAT 57
Qy      23 LeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArgPheLeuAlaArg 42
Db      58 TTTCAAGAAATCAGTCCGAGAGGAAACCGTTTTTTTATTCATCG-----AGG 105
Qy      43 AspArgAsnLeuMetTrpAsnGlyArgIleIlyIlyGlyArgIlyArgIlyArgTrpAsnPhe 62
Db      106 CATRGAAATTTGCTGCTCAATGAGAAATCAATAGAGT----- 144
Qy      63 GlySerLeuIleAlaAspProArgTyrSerCysLeuGlyIlySerArgTrpGluIlyGly 82
Db      145 -----GTTGAAAGCAAACTAATTAATGA 168
Qy      83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyIleMetThrValSer 102
Db      169 CGGAAATTTCTGTGACGCTGCTGCTAATTTGCTCACTCATCTGAGAACGAGCATGACA 228
Qy      103 SerGluIlyIlySerValTyrAspValValLeuIlyGlnAlaLeuValIlyAspGluLeu 122
Db      229 TCGAACAACATGCTATGATGATGTTTGAAGGAGGACGCTTGTGAAAGGCAACTG 288
Qy      123 ArgSerThrAspAspLeuGluValIlyProAspIleValAlaProGlyAsnLeuGlyLeu 142
Db      289 AGATCTACCAATAGATTAAGAAAGAAACCGGATATATCTATTCGCGGAATTTGGCTTG 348
Qy      143 LeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGlyTyrAlaIlyThrPheTyr 162
Db      349 TTGAGTGAACCATATGATGATGAGTGTGGAAGTATGTCCAGATATGCAAAAGACCTTTAC 408
Qy      163 LeuGlyThrIlyIlySerMetThrProGluArgArgAlaIleTrpAlaIleTyrValTrp 182
Db      409 TTGAAACTATGCTAATGACTCCGAGAGAAAGGGCTATCTGGCAATATATATATATG 468
Qy      183 CysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAla 202
Db      469 TGCAGAGAACAGATGAACCTTGTGATGGCCCAACGATCATATATATATATATATATAT 528
Qy      203 LeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeu 222
Db      529 CTAGATAGTGGGAAATAGGCTAGAGATGTTTTCATATGGGCGGCGCATTTGACATGCTC 588
Qy      223 AspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAsp 242
Db      589 GATGCTGCTTGTTCGATACAGTTTCTAATCTTCCAGTGTATATTCACCCATTCAGAAAT 648
Qy      243 MetIleGluGlyMetArgMetAspLeuTrpIlySerArgGlyArgIlyThrPheAspGluLeu 262
Db      649 ATGATTGAAGAAATCCGATATGACTTGGAAATTCGAAATCAAAAACCTTGACGAACTA 708
Qy      263 TyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282
Db      709 TACCTTATATGTTATATATGTTGCTGTGACGTTGGTGTGATGAGTTCATATATATATG 768

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QY	283	Leu AaP ProG uSer Ly Ala Thr Thr G uSer Val Tyr Asn Aa Ala Leu Ala Leu G Y	302
Db	769	ATG G C C C T G A T C A A G G C A A C A G A G C G T A T A T A T G C T T G C T G G G G	828
QY	303	Leu Aa enG In Leu Thr Asn I e Leu Ar g Asp Val G I G u Asp Ala Ar G Y Ar G	322
Db	829	ATG C A A T C A T T A C T A C A T C T G A G A G T G T G G A A A G T C C A G A G G A A	888
QY	323	Val Tyr Leu ProG In AspG Iu Leu Ala G In A aG I Leu Ser AspG Iu Asp I e Phe A	342
Db	889	G T C T A C T G C C T C A G A T G A T G C A G G C A G C G T C A T C G A T G A A T A T T G C T	948
QY	343	G I A r G A I Thr Asp Ly S Tr P Ar G Asp Phe Met Ly S G In I e G In A r G A I A r G Y S	362
Db	949	G G A G G G G A C G A T A A T G G A G A T C T T T G A A G A A C A A T A T G G C A G A A A G	1008
QY	363	Phe Phe AspG Iu SerG Iu Ly G I Y Ala Thr G Iu Leu Asp Ser Ala Ser Ar G Tr P ro Val	382
Db	1009	T T C T T G A T G A G G C A G A A T G G C T G C A A A T T G A C T C A G C T A G A T A T T C C T G T A	1068
QY	383	Leu Thr Ala Leu Leu Tyr Ar G Lys I e Leu AspG Iu eG Iu A Asn AspD Tyr Asn	402
Db	1069	T G G G C A T T G G C T T T A C C G C A A A T A C T A G T G A T T G A G C C A A G A C T A C A C	1128
QY	403	Asn Phe Thr Ar G A I A Tyr Val Ser Ly S P ro Ly S Leu Leu Thr Leu Pro I e Ala	422
Db	1129	A A C T T C A A A G A G C A T A T G T G A C A A T C A A A A G T T G A T G C T T A C T A T T G C A	1188
QY	423	Tyr Ala Ly Ser Leu Val Pro Pro Asn Ar G I hr Ser Ser	435
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RESULT 5
US-09-938-842A-729
: Sequence 729, Application US/0993842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kreps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: TITLE OF INVENTION: SAME, AND METHODS OF USE
: FILE REFERENCE: SCRIPT300-3
: CURRENT APPLICATION NUMBER: US/09/938,842A
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227,866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 729
: LENGTH: 1269
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-729

```

Alignment Scores:	
Pred. No.:	2,37e+183
Score:	1,542.00
Percent Similarity:	81.86%
Best Local Similarity:	72.11%
Query Match:	67.93%
DB:	10
	Gaps:
	8

```

Oy      1 MetSerMetSerValAlaLeuLeuTyrValVal-----SerProThrSerGluValSer 18
        |||||  |||||:::|||||
        |||||  |||||:::|||||
Db      1 ATGTCCTTCCTCGTAGCAGTGTAATGGGTGCTACTTCTTCTCMAATCCAGACCAATG 60

```

QY	19	hngclYthrgIyleuLeuAaspSerValArgclucIyasnArgValPheValSerSerArg	38
		:::-----	
Db	61	AACAATTGGGGTGGTA-----	99
		-----AGGGTCTCAAGATCTTCTAGA	
QY	39	PheLeu1laArgAapArgAsnLeuMetTrpAsnclYrgIlelySlysgly-GlyArggl	58
		:::-----	
Db	100	CTGTTCTTCCTTGTGAG-----	147
		-----AATAGAGACTTAAACAAAGGTAGAGAAG	
QY	58	narGTTrpAsnDheglSerLeu1lealAaspProArgTySerCysLeuglyGlySerAr	78
		:::-----	
Db	148	CAGATACCAACTTGAGTCTTCT-----	186
		-----TTGTAAGAACCGA	
QY	78	gThrgIuylsglySerThrPheSerValGlnSerSerleuValAaspProalagly	98
		:::-----	
Db	187	AGTAAAGAATT-GGTGT-----	239
		-----GTGCTTCAAGCTTAGTACCAAGTCTCTGGAGA	
QY	98	uMetThrValSerSerGlySlyIyValTyrAspValValLeuylsglnalaleuVal	118
		:::-----	
Db	240	GATAGCTCTTTCATCTGAGAGAGAGGTTTAAAGTGTGTGTGAACAAAGCTGTGGT	299
QY	118	llyArgTrlLeuArgSerThrAsp--AspLeuGlyVallys-----	135
		:::-----	
Db	300	GAACAACAGCTAAGGCTTCTTCTTATGACCTTGATGTGAAGAAACACAAGATGTGT	359
QY	135	lValProglYAsnLeuglyLeuLeuSerGluValATyrAspArgCysglYgluValCysAl	155
		:::-----	
Db	360	TCTTCCTGGAGTTTGAAGTTGTTGGGGAAGCTTATGATGATGAGCGGTGAAGTTGGC	419
QY	155	agluTyrAlaIysThrPheTyrLeuglyThrLysLeuMetThrProgluArgArgAl	175
		:::-----	
Db	420	TGAATATGCTAAGCGTTTATCTTGGAACTTGCTTATGACACCCGAAGCGAAAGGC	479
QY	175	alIleTrpAlaIleTyrValTyrCysArgArgThrAspGluLeuValAspIyProAsnAl	195
		:::-----	
Db	480	GATTTGGCAATCTAAGCTTGTGTGTAGAGACTGATGAATGTGTGATGGGCCAAATGC	539
QY	195	aseThiIleThrProgluAlaLeuAspArgTrpGluThrArgLeugluAspIlePheSe	215
		:::-----	
Db	540	TTCACTATTACTCCCATGGCTTATAGATAGATGGGAAGCAAGTTATAGAAGATCTTTCCG	599
QY	215	rgIyArgProPheAspMetLeuAspAlaIaleuSerAspThrValSerArgPheProVa	235
		:::-----	
Db	600	TGTCGTCTCTTCAGATATGCTTGAATGCTGCTCGCTGATACAGTGTGTAGATACCCGT	659
QY	235	lAspIleGlnProPheArgAspMetIlegluGlyMetArgMetAspLeuTrpIySerAr	255
		:::-----	
Db	660	CGAATATTCAGCAATTCGAGCAATGCAATCGAAGATAGAAATGCACTTGAAGAAATCGAG	719
QY	255	gTyrIysThrPheAspGluLeuTyrLeuTyrCysTyrTyrValAlaglyThrValGlyLe	275
		:::-----	
Db	720	ATACCAAGACTTCATGATCTATACCTTACTCTGCTACTACCTCGCTGAAACCGTGGATT	779
QY	275	uMeSerValProValMetGlyIlealAProgluSerLysAlaThrThrgIuSerValTy	295
		:::-----	
Db	780	GATAGAGCTTCGGTATGAGGAATCGATCCCTAATCGAAGCAACCAACCGAATGTTTTA	839
QY	295	rAsnAlaIaleuAlaleuglyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGl	315
		:::-----	
Db	840	CAAGCGTCCCTGGCCCTTGGTATAGCCAAATCAACTTAACTACTCAGAGACGTAGAG	899
QY	315	YgluAspAlaArgArgGlyArgValTyrLeuProgluAspGluLeuAlaglnalaglyLe	335
		:::-----	
Db	900	CGAAGATGCGAAGAGAGAGGTTTATCTGCTCTAGAGATGAATTTGGCTCAGGCTGGCT	959
QY	335	uSerAspGluAspIlePheAlaglyArgValThrAspLysTrpArgAsnPheMetLysLy	355
		:::-----	
Db	960	TTTCAGATTAACAATATTCGCCGGAAGAAAGTACATGATTAATGCGAAGAACTTCATGAAT	1019
QY	355	sgInIleGlnArgAlaArgLysPhePheAspGluSerGluylsglyValThrgIuLeuAs	375
		:::-----	
Db	1020	GCACCTTAAACAGCAAGAAATGTTCTTCGACGAAGTGAAGAAAGGCTTCACCGAGCTCAG	1079

Db 1020 GCAGCTTAAACGACGACGAGATGTTCTTTCGACGAGCTGAGAAAGCCGTCCACCGAGCTAG 1079

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Qy 375 pserAlaSerArgTTPProValLeuThraAlaLeuLeuTyrArgLysIleLeuAspG1 395
Db 1080 TCCTCCAGACAGATGGCGCTTATGGGCTTATGCTATGTTACAGAGAACTACTGACGA 1139
Qy 335 UllLeuLalaasnApyrYraasnAphethrArgArgAlaTyrValSerLysProLysL 415
Db 1140 GATTAAAGCGAATGATTCACAAATTTTAACTAAGAGAGCTTATGCGGGAAGTCMAA 1199
Qy 415 sleuLeuThraLeuProIleAlaTyrAlaLysSerLeuValProProAsnArgThrSerSe 435
Db 1200 AATTCCAGCTTTCCTTATGGCTTATGCTTAATCACTACTA-----AGACTTCAAG 1250
Qy 435 r 435
Db 1251 T 1251

RESULT 6
US-10-149-759-53
; Sequence 53, Application US/10149759
; Publication No. US20030157592A1
; GENERAL INFORMATION:
; APPLICANT: Lerchl, Jens
; APPLICANT: Renz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reinold, Andreas
; APPLICANT: Cirus, Petra
; TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins
; TITLE OF INVENTION: involved in the synthesis of tocopherols and
; FILE REFERENCE: BASF/NAE 1333/99 PCT/US
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/10/149,759
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: WordPerfect version 6.1
; SEQ ID NO 53
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Physcomitrella patens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(397)
; OTHER INFORMATION: 02_ppprocl_046_a07rev
US-10-149-759-53

Alignment Scores:
Pred. No.: 9,34e-49 Length: 684
Score: 468.00 Matches: 93
Percent Similarity: 82.31% Conservative: 14
Best Local Similarity: 71.54% Mismatches: 23
Query Match: 20.62% Indels: 0
Gaps: 0

US-09-847-081b-2 (1-440) x US-10-149-759-53 (1-684)
Qy 310 ILeuLeuArgAspValGlyGluAspAlaArgArgGlyArgValTyrLeuProGlnAspGlu 329
Db 5 ATCTGAGGAGATGTTGAAGAAAGATGACGCCGTGGAGAGTATACCTCCACAGATGAA 64
Qy 330 LeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGlyArgValThrAspLysTrp 349
Db 65 CTGGCAGCTTTCGGTCTGTGCGATGACAGCATTTTTCGGAAGATTACTGATAATG 124
Qy 350 ArgAsnPheMetLysLysGlnIleGlnArgAlaArgLysPhePheAspGluSerGluLys 369
Db 125 AGGCGATTTCATGAAGACCAATTAAGAGCTAGAGTCTTCTTGTGAGGCTGAGAAA 184
Qy 370 GlyValThrGluLeuAspSerAlaSerArgTTPProValLeuThraAlaLeuLeuTyr 389
Db 185 GGTGTACGTGACGTGACAAAGACAGCTGCTGCTGTGTGCTGCGCTTCACTTCTTAC 244
Qy 390 ArgLysIleLeuAspGluIleGluAlaasnApyrYraasnAphethrArgArgAlaTyr 409

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Db 245 CAGCAAAATTCGACGCGCATTGAAAGCCAGATTACATTACTTCAAAAAGAGCTTAC 304
Qy 410 ValSerLysProLysLysLeuLeuThraLeuProIleAlaTyrAlaLysSerLeuValPro 429
Db 305 GTAGCAAGAGGGAAGAAAGAGCTTCTTCTTACTTATGCTTATGAGAGAGCTTGTCCA 364
Qy 430 ProAsnArgThrSerSerProLeuAlaLys 439
Db 365 CTTCAGATGACCTTCCAGGTTAGACGT 394

RESULT 7
US-10-156-761-1013
; Sequence 1013, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMBURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1013
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1026)
US-10-156-761-1013

Alignment Scores:
Pred. No.: 2,04e-36 Length: 1026
Score: 372.00 Matches: 101
Percent Similarity: 51.75% Conservative: 47
Best Local Similarity: 35.31% Mismatches: 116
Query Match: 16.39% Indels: 22
Gaps: 7

US-09-847-081b-2 (1-440) x US-10-156-761-1013 (1-1026)
Qy 143 LeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyr 162
Db 46 CTGGCAAGGCTTACACGCACTGCGCGCGCTCAACGCGGCAAGCAAGCTTCTTC 105
Qy 163 LeuGlyThrLysLeuMetThrProGluArgArgAlaIleThrPalaIleTyrValTyr 182
Db 106 CTCGCCACACAGATGCTGCGCGCTGCAAGCGCGCGCGCGCGCGCTTACAGATTTC 165
Qy 183 CysArgArgThrAspGluLeuValAsp-----GlyProAsnAlaSer 196
Db 166 GCACGCTGGCGCGACGATGTCGACTCCCTGGACACCAACCGTGGCCCC----- 216
Qy 197 HisIleThrProGlnAlaLeuAspArgTTPGluThrArgLeuGlu---AspIlePheSer 215
Db 217 GCTGTGCTCTGCGGCGGCTGCGCGCTTCCAGAGAGCTTCCGAGCGGAGCTCGTAG 276
Qy 216 GlyArgProPheAspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProVal 235
Db 277 GGAACACGACCAAGCGCGTGTCTGCGCTGCGCGAGACGCGCGCGGTACGCATC 336
Qy 236 AspIleGlnProPheArgAspMetIleGluGlyMetArgMetAspLeuTTPLysSerArg 255

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337	GACGACACGACGACTTCAGTACCTTCATGACGGCAGGACGACGACGACCTCGAGGCTCACCCGC	336
QY	256 TyrLysThrPheaspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeu	275
Db	397 TACGAGACTTACGCCGACCTGCGCGGAGCTCATACACGGTTTCCGCCCGGAGATCGGGCTG	456
QY	276 MetSerValProValMetGly---IleValProGluSerLysValAlaThrThrGluSerVal	254
Db	457 CAGATGCTCCGGTGTCTGGAGACCGTGTCGCCGCTGAGGAGGCCGACCCAC-----	510
QY	295 TyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGluLeuThrAsnIleLeuArgAspVal	314
Db	511 -----GCCGCGCGCCCTGGGAGAGTGGCGCTTCCACTGACCAACTTCTCGCGGACGTG	561
QY	315 GlyGluAspAlaArgArgGlyArgValTyrLeuProGluAspGluLeuAlaGlnAlaGly	334
Db	562 GCGGAGAGACCTGAGACCGCGGCGCGCTCTACTGCCGCGACCTGTTTGGCGGCCACCGC	621
QY	335 LeuSerAspGluAspLysPhe-----AlaGlyArgValThrAspLysTrp	349
Db	622 GTC---GACCGGAGACTGCTGCGCTGAGACGAGACACCGCGCGCGGACCCGCGATC	678
QY	350 ArgAsnPheMetLysLysGlnIleGlnArgAlaArgLysPheAspGluSerGluLys	369
Db	679 ACCCTGCGCCTCAAGGCCCTTGAGGGCTGACCCCGGCTGTGTAACCGCAGGCGCGCCG	738
QY	370 GlyValThrGluLeuAspSerAlaSerArgTrpProValLeuThrAlaLeuLeuTyr	389
Db	739 GGGCTTTCGACTCTGACCCCGGTGGCGCGCGCTGATCCGACGGGGTTTGGTGTGTAC	798
QY	390 ArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsnAsnPheThrArgAlaGlyTyr	409
Db	799 GCGGAGATCTCTGACGCCATCGCCGACGACGGGTACGGGTCTGTCCACCGCGTCCGTG	858
QY	410 ValSerLysProLysLys 415	
Db	859 GTGCCGCGCGCGCGCT 876	
RESULT 8		
US-10-156-761-1		
; Sequence 1, Application US/10156761		
; Publication No. US20030119018A1		
GENERAL INFORMATION:		
; APPLICANT: OMURA, SATOSHI		
; APPLICANT: IKEDA, HARUO		
; APPLICANT: ISHIKAWA, JUN		
; APPLICANT: HORIKAWA, HIROSHI		
; APPLICANT: SHIBA, TADAYOSHI		
; APPLICANT: SAKAKI, YOSHIYUKI		
; APPLICANT: HATTORI, MASAHIRA		
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES		
; FILE REFERENCE: 249-262		
; CURRENT APPLICATION NUMBER: US/10/156, 761		
; PRIOR FILING DATE: 2002-05-29		
; PRIOR APPLICATION NUMBER: JP 2001-204089		
; PRIOR FILING DATE: 2001-05-30		
; PRIOR APPLICATION NUMBER: JP 2001-272697		
; PRIOR FILING DATE: 2001-08-02		
; NUMBER OF SEQ ID NOS: 15109		
; SEQ ID NO 1		
; LENGTH: 9025608		
; TYPE: DNA		
; ORGANISM: Streptomyces avermitilis		
; FEATURE:		
; NAME/KEY: misc feature		
; LOCATION: (4187715)		
; OTHER INFORMATION: a, t, c, g, other or unknown		
US-10-156-761-1		
Alignment Scores:		
Pred. No.:	2,596-30	Length: 9025608
Score:	372.00	Matches: 101
Percent Similarity:	51.75%	Conservative: 47

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Best Local Similarity: 35.31% Mismatches: 116
Query Match: 16.39% Indels: 22
Db: 15 Gaps: 7

US-09-847-081B-2 (1-440) x US-10-156-761-1 (1-9025608)

QY 143 LeuSerGluAlaTYrAspArgCYeGlyGluValCYeAlaGluTYrAlaLYrThrPheTYr 162
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1291845 CTGGCGAAGGCTTACACGCACTGCCGCCGCTCAACCGCGGACCGCAAGACTACTTC 1291904
QY 163 LeuGlyThrLYrLeuMetThrProGluArgArGAlaIleThrAlaIleTYrValTYr 182
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1291905 CTGCCCACTCAACTCTGCTCCGCTGCAAGCGCGCGCCCGCTGACGCGCTTACGAGATTC 1291964
QY 183 CysArgArgThrAspGluLeuValAsp-----GlyProAsnAlaSer 196
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1291965 GCACGCTGGGGCCGACGACATCGTGAATCCCTGGACACCAACCGTGGCCCC----- 1292015
QY 197 HisIleThrProGluAlaLeuAspArgTYrGluThrArgLeuGlu---AspIlePheSer 215
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1292016 GCTGTGGCTCGCGCGGCGCTCGCGCCGCTCAGAGAGACCTTGGGACGCGGACGCTGAG 1292075
QY 216 GlyArgProPheAspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProVal 235
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1292076 GGACACACGACACCGGCGCGGCTGCTGCGCTCGCGACGAGCGCGCGCGTACGCATC 1292135
QY 236 AspIleGlnProPheArgAspMetIleGluGlyMetArgMetAspLeuTYrPlysSerArg 255
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1292136 GACCAACACGACCTTCACTGATCTTCAACGCGCATGCGGACGACCTGAGAGCTCACCGGC 1292195
QY 256 TYrLYrThrPheAspGluLeuTYrLeuTYrCYeTYrTYrValAlaGlyThrValGlyLeu 275
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1292196 TACACAGACTACACGCGGACCTGCGGCTACATGACACGTTGCGCGCGCGTATCGGCGCTG 1292255
QY 276 MetSerValProValMetGly---IleAlaProGluSerLYrAlaThrThrGluSerVal 294
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1292256 CAGATGCTGCGGCTGCTGGGACCGGTGCTCCGCTGAGAGAGGCGCGCACCCAC----- 1292309
QY 295 TYrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspVal 314
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1292310 -----GCGGCGGCGCTCGGAGTGGCTTCCAGCTGACCAACTTCTTCCGGAGCTG 1292360
QY 315 GlyGluAspAlaArgArgGlyArgValTYrLeuProGlnAspGluLeuAlaGlnAlaGly 334
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1292361 GCGCAGAGACTGACCGCGCGCGGCTCTATCTGCGCGCGACCTGTTGCCGCCACCGGC 1292420
QY 335 LeuSerAspGluAspIlePhe-----AlaGlyArgValThrAspLYrTrp 349
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1292421 GTC---GACCGGACCTGCTGCTGCGCTGAGCAGGAGACACCGCGCGCGGACCGCGATTC 1292477
QY 350 ArgAsnPheMetLYrLYrGlnIleGlnArgAlaArgLYrPhePheAspGluSerGluLYs 369
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1292478 ACCCGTCCGCTCAAGCGCGCTTGAAGGCGCTAACCGCGGTGTATACCGCAGAGCGCGCGC 1292537
QY 370 GlyValThrGluLeuAspSerAlaSerArgTYrProValLeuThrAlaLeuLeuLeuTYr 389
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1292538 GCGCTTCCGATGCTCGACCGCGTGGCGCGCCCGCGCATCCGACCGGGCTTCCGTCGTAC 1292597
QY 390 ArgLYrAlaLeuAspGluIleGluAlaAsnAspTYrAsnAsnPheThrArgAlaTYr 409
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1292598 GCGCGGATCTCTGACGCGCATTCGCGACGAGGAGTACCGGTGTCTCACCGCGTGCCTG 1292657
QY 410 ValSerLYrProLYrLYs 415
||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 1292658 GTGCCGCGCGCGCGCT 1292675

RESULT 9
US-10-156-761-1642
; Sequence 1642, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMDRA, SATOSHI
; APPLICANT: IKEDA, HARUO

```

APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIYUKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 1642
 LENGTH: 948
 TYPE: DNA
 ORGANISM: Streptomyces avermitilis
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(948)
 US-10-156-761-1642

Alignment Scores:
 Pred. No.: 5,766-36 Length: 948
 Score: 368.00 Matches: 96
 Percent Similarity: 52.45% Conservative: 43
 Best Local Similarity: 36.23% Mismatches: 104
 Query Match: 16.21% Indels: 22
 Gaps: 6
 DB: 15
 US-09-847-081b-2 (1-440) x US-10-156-761-1642 (1-948)

Oy 146 AlAtyrraspargCyGgLygluValCyAlaGluTyrAlaYsrThrPheTyrLeuGlyThr 165
 Db 52 GCATACAGCTACTGCGAGACCGTCAACCGGCGAGCGGCCGCACTTGCTGCTACGCGATC 111
 Oy 166 LysLeuMetThrProGluArgArgArgAlaIleTTPAlaIleTyrValTTPCyArgArg 185
 Db 112 AGCGTGTGCGCGACGCCCGCAAGCGCGCGCGATGCGCGCTTACGCTTCCGCGCGCC 171
 Oy 186 ThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArg 205
 Db 172 GTCGACGACATCGCGAGCGCGCGCTCGCGCGACGTGAAGCGCGAGCGCTCGAGGAC 231
 Oy 206 TrpGluThrArgLeuGluAspIlePheSerGlyArg-----ProPheAspMet 221
 Db 232 ACCCGGGCGTGTGCTGCCGGGTGCGTGAACGGCGGTGAGCAGACGACGACGCC 291
 Oy 222 LeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArg 241
 Db 292 GTCGCGGTGCGCTTGGCGACGCGCGCGAGCGAGCTTCCGATCCGCTCGCGCGCTCAGC 351
 Oy 242 AspMetIleGluGlyMetArgMetAspLeuTyrPlySerArgTyrTyrThrPheAspGlu 261
 Db 352 GAATGATGACGAGCGGTGCTCATGACGTGCGCGCGCGAGCAGACTTACGAGACCTGGAGCAG 411
 Oy 262 LeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMet 281
 Db 412 CTCAGAGTCTACTGCGCTGTGTGCGACGGCGACCGCGGCTGCTGCTGCGCTGCTTC 471
 Oy 282 GlyIleAlaProGluSerValaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeu 301
 Db 472 GGCACGGAACCG 528
 Oy 302 GlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGly 321
 Db 529 GAGCTGTGCTTCCACTCACCACCAACCTCCGCGAGCGTGAAGCGCGCGCGCGCGCG 588
 Oy 322 ArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSer-----AspGlu 338
 Db 589 GCGACATCTATGCGCGCGCGCGAGCAGCTCGCAAAATTGCGCTGCTGCGCGCGGTTCAGCCG 648

Oy 339 AspIle-----PheAlaGlyArgValThrAspLysTTPArgAspPhe 352
 Db 649 CCAGTCCACCGAGGAGGATCGCACTTGCGCGGCGCTGCTG-----CACTTC 693
 Oy 353 MetLysLysGlnIleGlnAlaArgLysPheAspGluSerGlyValThr 372
 Db 694 -----GAGGCGCTCGCGCGCGCGCGCGCTTTCGCCAGCGGCTACCGGCTGCTCCC 744
 Oy 373 GluLeuAspSerAlaSerArgTTPProValLeuThrAlaLeuLeuLeuTyrArgLysIle 392
 Db 745 ATGCTGAGACCGCGCGCGCGCGCGCTGCTGTGCGCGCGATGCGGCGCATCTACCGCGGCTC 804
 Oy 393 LeuAspGluIleGlu 397
 Db 805 CTCGATCGCATCGAG 819

RESULT 10
 US-10-156-761-1/c
 Sequence 1, Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMIURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIYUKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 1
 LENGTH: 9025608
 TYPE: DNA
 ORGANISM: Streptomyces avermitilis
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (4187715)
 OTHER INFORMATION: a, t, c, g, other or unknown
 US-10-156-761-1

Alignment Scores:
 Pred. No.: 8,246-30 Length: 9025608
 Score: 368.00 Matches: 96
 Percent Similarity: 52.45% Conservative: 43
 Best Local Similarity: 36.23% Mismatches: 104
 Query Match: 16.21% Indels: 22
 Gaps: 6
 DB: 15
 US-09-847-081b-2 (1-440) x US-10-156-761-1 (1-9025608)

Oy 146 AlAtyrraspargCyGgLygluValCyAlaGluTyrAlaYsrThrPheTyrLeuGlyThr 165
 Db 2025896 GCATACAGCTACTGCGAGACCGTCAACCGGCGAGCGGCCGCACTTGCTGCTACGCGATC 2025837
 Oy 166 LysLeuMetThrProGluArgArgArgAlaIleTTPAlaIleTyrValTTPCyArgArg 185
 Db 2025836 AGCGTGTGCGCGACGCCCGCAAGCGCGCGCGATGCGCGCTTACGCTTCCGCGCGC 2025777
 Oy 186 ThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArg 205
 Db 2025776 GTCGACGACATCGCGAGCGCGCGCTCGCGCGACGTGAAGCGCGAGCGCTCGAGGAC 2025717
 Oy 206 TrpGluThrArgLeuGluAspIlePheSerGlyArg-----ProPheAspMet 221
 Db 2025716 ACCCGGGCGTGTGCTGCCGGGTGCGTGAACGGCGGTGAGCAGACGACGACGCC 2025657

QY	222	LeuApSPaLaLaLeuSerAAspThrValSerArgPheProValAspLIeGlnProPheArg	241
Db	2025656	GTCCGGCTGCGCCCTGGGCCACGCGCCGACGAGTTCCTCCGATCCGCGCTGGCGGCTCGAC	2025597
QY	242	AspMetLIeGIuGIyMeTArgMeTAspLeuTrpLysSerArgTYrLysThrPheAspLIu	261
Db	2025596	GAACGTATCGACCGCGCTCCTCATGAGCGTGGCGCGGACGACCTACGACACTTGGGACGAC	2025537
QY	262	LeuTYrLeuTYrCysTYrTYrValAlaGlyThrValGlyLeuMetSerValProValMet	281
Db	2025536	CTCAAGGCTCTACTGCGCGCTGTGTGGCAGAGGGCCATCGGCGCGCTTCGCTCGCGGTTC	2025477
QY	282	GlyLIeAlaProGluSerLysAlaThrThrGluSerValTYrAsnAlaLaLeuAlaLeu	301
Db	2025476	GGCACGGAACGGGGCGCCGGCGC--GCCAGCGCGCGTACGAGTACGCGACCTTC	2025420
QY	302	GlyLeuAlaAsnGlnLeuThrAsnLIeLeuArgAspValGlyGlyAspAlaArgArgGly	321
Db	2025419	GGCCTCGCTCTCCAGCTACACCACTCTCCGCGACGTAACCGAGACGCCGAGGGCGGC	2025360
QY	322	ArgValTYrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSer-----AspGlu	338
Db	2025359	CGCACCTATCTGCGCGCGCGACCTCGCCAAATTGCGCTGCGCGCGGTTGACCGG	2025300
QY	339	AspLIe-----PheAlaGlyArgValThrAspLysTrpArgAsnPhe	352
Db	2025299	CCGATCCACCGAGGAGTCCGACTCTGGGGCGCTCGG-----CACTTC	2025255
QY	353	MetLysLysGlnLIeGlnArgAlaArgLysPheAspGluSerGlyValThr	372
Db	2025254	-----GAAATCGCTCGGGCCCGCCCTTTTCGCGAGGGCTACCGGCTGCTGCC	2025204
QY	373	GluLeuAspSerAlaSerArgTrpProValLeuThrAlaLeuLeuTYrArgLysLIe	392
Db	2025203	ATGCTGGACCGCGCGAGCGGTGCTGTGCGCGGATGCGGGGATTAACGCGGCTC	2025144
QY	393	LeuAspGluLIeGln	397
Db	2025143	CTCGATCGCATCGAG	2025129
RESULT 11			
US-10-128-713A-15			
US-Sequence 15, Application US/10128713A			
Publication No. US20030170847A1			
GENERAL INFORMATION:			
APPLICANT: Bramucci, Michael G			
TITLE OF INVENTION: Genes Involved in Isoprenoid Compound Production			
FILE REFERENCE: CI-1788			
CURRENT APPLICATION NUMBER: US/10/128,713A			
CURRENT FILING DATE: 2002-04-22			
NUMBER OF SEQ ID NOS: 36			
SOFTWARE: Microsoft Office 97			
SEQ ID NO 15			
LENGTH: 945			
TYPE: DNA			
ORGANISM: Rhodococcus erythropolis			
US-10-128-713A-15			
Alignment Scores:			
Pred. No.: 6 71e-35 Length: 945			
Score: 359.50 Matches: 99			
Percent Similarity: 48.66% Conservative: 46			
Best Local Similarity: 33.22% Mismatch: 116			
Query Match: 15.84% Indels: 37			
DB: 13 Gaps: 8			
US-09-847-081B-2 (1-440) x US-10-128-713A-15 (1-945)			
QY	140	LeuGlyLeuLeuSerGluAlaTYrAspArgCysGlyGluValCysAlaGluTYrAlaLys	159
Db	1	ATGAACGATTTGTCTGCGCTCTATTAATTCTGCGAGACGTGACGAGGAACACGCGCGA	60
QY	160	ThrPheTYrLeuGlyThrLysLeuMetThrProGluArgArgAlaLIeTrpAlaLIe	179

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Db      61  AGGATCTTCTGGCCACTCGGTGCTGCCCGAGCCTCGACGCGCGGACGTTCCAGCTCTC 120
Qy      180  TyrValTrrCyArGrArGrThrAspGluLeuValAspGlyProAsnAlaSerHis----- 197
Db      121  TACGATTTGCTCGCGCTCGACGACGCTGCTGAGCAACCTCGGCTCCCATGAACGA 180
Qy      198  -----1IethProGlnAlaLeuAspArgTrrGluThr 208
Db      181  GGACAGGTCTCGCCGACGCTGCACGCTGACGCCGTCAACCCGACCTCGAACAC---CCCACT 237
Qy      209  ArgLeuGluAspLlePheSerGlyArgProPheAspMetLeuAspAla-----AlaLeu 226
Db      238  GCGACAGGTGGCTTCCCGCTCGACGATTCCTCTGACCTTGACACCGCTACTCTCCGCTTC 297
Qy      227  SerAspThrValSerArgPheProValAspLleGlnProPheArgAspMetLleGluGly 246
Db      298  GCCGATGCTGTGAAGACGTTCCGACATTCGCCCGGTCAACTTCGACGCGCTTCTTGAGTCC 357
Qy      247  MetArgMetAspLeu-----TrpLysSerArgTyrLysThrPheAspGlu 261
Db      358  ATGCGGATGAGCGCCCGCACACCGGAGAGTTGACCCGCTCTCAACACGATGAGCGAG 417
Qy      262  LeuTyrLleuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMet 281
Db      418  CTTCGCGAGTACATGATGACGCTCCGCGCTGCTCATCGTTTGACAGATGCTCCGATTCCTC 477
Qy      282  GlyIleAla---ProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAla 300
Db      478  GGAGTGAGCGCTTCCGACGACGAGAGCTGTAAGT-----CCGCGCTGCAGAT 522
Qy      301  LeuGlyLeuAlaAsnGlnLeuThrAsnLleLeuArgAspValGlyGluAspAlaArgArg 320
Db      523  CTGCGTGAGGCGCTTTCAGCTGACCACTTCATCCGCGACGCTCGGTGAAGACTCGACCG 582
Qy      321  GlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspLle 340
Db      583  GGACGCTGTATCTCCCGCGGCGCGAGTTGCGCGCATTCGCGGGTGCACATCGAGATGCTC 642
Qy      341  PheAlaGlyArgValThrAspLysTrrPArgAsnPheMetLysGlnLleGlnAlaArgAla 360
Db      643  GAGCAGCGGCGCGAGAAC-----GGAAGGTGACGCTCGGCTCAACGCGCGCG 690
Qy      361  -----ArgLysPhePheAspGluSerGlyLysGlyValThr 372
Db      691  CTGGCACACTTCATTCAGCTGACGTACGCGGGGCGGTATCGGCGCGAATCGCGATCCCG 750
Qy      373  GluLeuAspSerAlaSerArgTrrProValLeuThrAlaLeuLeuLeuTyrArgLysLle 392
Db      751  ATGCTCGATTCGCGGGGTCCAGCGCTGATCCGACGACGCTTTCGTTGTGTGCGAGCAATT 810
Qy      393  LeuAspGluLleGluAlaAsnAspTyrAsnAsnPheThrArgArgAlaTyrVal 410
Db      811  CTGACACAGGTGAGCGCGCGCTTCGCGATCTCGCATGACGAGTGTCCGTT 864

RESULT 12
; Sequence 1, Application US/10041472
; Publication No. US20020092039A1
; GENERAL INFORMATION:
; APPLICANT: Shemake, Christine
; TITLE OF INVENTION: METHODS FOR PRODUCING CAROTENOID COMPOUNDS AND SPECIALITY OILS IN
; FILE REFERENCE: 16516, 141
; CURRENT FILING DATE: 2002-01-10
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: US 08/908758
; PRIOR FILING DATE: 1996-09-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1

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LENGTH: 1232
 TYPE: DNA
 ORGANISM: Echinia uredovora
 US-10-041-472-1

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 1.37e-33	1232	350.50	110	55	162	49
Percent Similarity: 43.88%						
Best Local Similarity: 29.25%						
Query Match: 15.44%						
DB: 14						11

US-09-847-081b-2 (1-440) x US-10-041-472-1 (1-1232)

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Oy 77 SerArgThnGluLysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAla 96
Db 83 AGCCGTCCTTGAAGGCGG-----CAATCCGCGCAGTGGCTTCATTCCGCGC 127
Oy 97 Gly-----GluMetThrValSerSerGluLysValTyrAspValValLeuLysGln 114
Db 128 GGCCTCAATCATCATGATGATCCAGAGAAAGGTC----- 166
Oy 115 AlaAlaLeuValLysArgGlnLeuArgSerThrAspAspLeuGluValLysProAsp 133
Db 167 -----AACACTGACATTACTTCATTACCAAGCAATGGT 199
Oy 134 -----IleValValProGluLysLeuGlyLeuLeuSerGluAlaTyrAspArgGly 151
Db 200 GGAGAGATGAAGTGAATGATGATATCCGCTGTTACTCAATCATGCGGTC----- 247
Oy 152 GluValCysAlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGlu 171
Db 248 GAAAGAGATGCGAGTGGCGCGAAAGCTTTGGACAGACCTCAAGTTATTGATGCAAAA 307
Oy 172 ArgArgArgAlaIleTyrAlaIleTyrValTyrCysArgArgThrAspGluLeuValAsp 191
Db 308 ACCCGCGGAGCGTACTGATGCTTACGCGTGGTCCGCGCATTTGACATGATTTATGAC 367
Oy 192 GlyProAsn-----AlaSerHisIleThrProGlnAlaLeu 203
Db 368 GATCAAGCGCTGGCTTTCAGCGCGCGCGAGCTGCTTACAAACCCGCAACAGCTGCG 427
Oy 204 AspArgTyrGluThrArgLeuGluLysIlePheSerGly---ArgProPheAspMetLeu 222
Db 428 ATGCAACTTGATGAATAAAGCGCGCATGATGACAGATTCACAGATGACAGAACCGCG 487
Oy 223 AspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArg--- 241
Db 488 TTTCGGGCTTTTCAGGAAGTGGCTATGCTCAT-----GATATCGCCCGGCTTACCG 541
Oy 242 ---AspMetIleGluGlyMetArgMetAspLeuTyrPheSerArgTyrLysThrPheAsp 260
Db 542 TTTCATCATCTGAAAGGCTTCCGCAATGATGATGACGAGCCCAATATACGCCAAGCTGAT 601
Oy 261 GluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProVal 280
Db 602 GATACGCTGCGCTATTCATTCATCATGTCGAGCGCTTTCGCTTATGATGCGCAATC 661
Oy 281 MetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAla 300
Db 662 ATGGGCGTG-----CGGATTAACGCCACGCTGAC-----CGGCGCTGTGAC 703
Oy 301 LeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuAlaGspValGlyGluAspAlaArgArg 320
Db 704 CTTCGGCTGCGATTTCAGTTGACCAATATTCCTCGGATATTCGACATTCGCGATGCG 763
Oy 321 GlyArgValTyrLeuProGluLysGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle 340
Db 764 GGCCTGCTTATCTGCGCGCAAGCTGCGTGCATGAAGGTCCTGAACAAGAAATATAT 823
Oy 341 PheAlaGlyArgValThrAspLysThrArgAsnPheMetLysGlnIleGlnArgAla 360

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Db 824 CGCGACCTGAAACCCTCAGCGCGCTGAGCCGATCGCCGCTGTTGGTCAGAAACA 883
Oy 361 ArgLysPhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTyr 380
Db 884 GAACCTTACTTATTTGTCTGCGACAGCGCGCTGCGAGAGTTGCCCCCGCTCCGCTCG 943
Oy 381 ProValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAsp 400
Db 944 GCAATCGCTACGGCGAAGCAGGATTCACGGAATAATAGTGTCAAAGTTGAACAGCCGCT 1003
Oy 401 TyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrPro 420
Db 1004 CAGCAAGCTTGGATGATCAGCGCGAGTCAACAGCCGCAAAATTAACGCTGCTGCTG 1063
Oy 421 IleAlaTyrAlaLysSerLeuValProProAsnArgThrSerSerPro 436
Db 1064 GCGGCTCTGTCTCAGGCTTACTTCCCGATGCGGAGCTATCTCTCC 1111

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RESULT 13

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US-09-941-947A-33
; Sequence 33, Application US/09941947A
; Publication No. US20030003528A1
; GENERAL INFORMATION:
; APPLICANT: Brzostowicz, Patricia C.
; APPLICANT: Cheng, Qiong
; APPLICANT: DiCosimo, Deana J.
; APPLICANT: Koffas, Mathios
; APPLICANT: Miller, Edward S. Jr.
; APPLICANT: Odum, J. Martin
; APPLICANT: Picataggio, Steve
; APPLICANT: Rouviere, Pierre E.
; TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
; FILE REFERENCE: C11903 US NA
; CURRENT APPLICATION NUMBER: US/09/941,947A
; CURRENT FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,858
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Pantoea stewartii
; US-09-941-947A-33

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Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score: 4.77e-32	891	336.50	88	52	131	19
Percent Similarity: 48.28%						
Best Local Similarity: 30.34%						
Query Match: 14.82%						
DB: 11						6

US-09-847-081b-2 (1-440) x US-09-941-947A-33 (1-891)

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Oy 158 AlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTyr 177
Db 13 TCGAAGAGCTTTGGAGCTGATCGACCTTTTCAGCCCAAAACCGGTCGAGGCTGCTG 72
Oy 178 AlaIleTyrValTyrCysArgArgThrAspGluLeuValAspGlyProAsn----- 194
Db 73 ATGCTTACGATGATGTCGCGCATGCGACACACTCATTCAGATCAAAACACTGGGCTTT 132
Oy 195 -----AlaSerHisIleThrProGlnAlaLeuAspArgTyrGluThrArg 209
Db 133 CATGCCAGCAGCCCTTCGACAGATGCTGACAGCGCGCTGACGAGCTTGAATGAATA 192
Oy 210 LeuGluAspIlePheSerGly---ArgProPheAspMetLeuAspAlaAlaLeuSerAsp 228
Db 193 ACGGCTCAGGCTTACGCGGCTTTCGCAATGACAGAGCCGCTTTCGCGGCTTTCAGGAG 252

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; FILE REFERENCE: 1721-55
; CURRENT APPLICATION NUMBER: US/10/166,037
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/297,272
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 4
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: crtb
; US-10-166-037-4

Alignment Scores:
Score: 7.81e-31 Length: 1008
Percent Similarity: 327.50 Matches: 99
Best Local Similarity: 45.68% Conservative: 49
Query Match: 30.56% Mismatches: 137
DB: 15 Gaps: 39

US-09-847-081b-2 (1-440) x US-10-166-037-4 (1-1008)

QY 139 AsnLeuGlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAla 158
DB 22 CATCTGGGCGCGCTGAGCGAGCCCTCATCCCGAACGCGC-----TCG 63

QY 159 LysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTyrAla 178
DB 64 AAGAGTTTCGACGCGCATCCAGCTGTTCCGATCCCGACCCGACCGCGTGCACCTG 123

QY 179 IleTyrValTyrPyrArgArgThrAspGluLeuValAspGly----- 192
DB 124 CTCTACGCTGCTGCTGCGGATTCGACATCGACGACGACGATCTCGAATTGCG 183

QY 193 -----ProAsnAlaSerHisIleThrProGlnAlaLeu--AspArgTrp 206
DB 184 CAGGCGCTCGGCGCGCTGCGCCGACATCGGACTTTGCAAGATGCTGCGGACGACGAC 243

QY 207 GluThrArgLeuGluAspIlePheSerGlyArgProPhe--AspMetLeuAspAlaIa 225
DB 244 GCGCAGCGCTGAG-----GGGCGCGCATGCGCGATCCGATGTCAGGGA 291

QY 226 LeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGlu 245
DB 292 TTGACGCGCTGTCGACGACGACGATTCGACCATCAGCTGTCGAGCTGCTGAC 351

QY 246 GlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeuTyrLeuTyr 265
DB 352 GGTCTCGCATGATGATGTCGACGCGCGCATTCGACGCGCTGAGGACGCTGACTAC 411

QY 266 CysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaPro 285
DB 412 TGCTATCAAGTGGCGCGCTGCTGCGCGATGATGTCGCGCATCATGAGC----- 462

QY 286 GluSerLysAlaThrThrGluSerValTyrAsnAlaIleAlaLeuAlaLeuGlyLeuAlaAsn 305
DB 463 -----GCTCGGAGAGGCGACGCTGACCGCGCGCGCATCTCGGATCTCGCGCTG 513

QY 306 GlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgIleArgValTyrLeu 325
DB 514 CAGCTCACCAACATGCGCGCTGATCGAGATGCCGACGCGCGCATGATCTG 573

QY 326 ProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGlyArgVal 345
DB 574 CCGCAGCATGCTGTGCGAGCGCGCGCGCGCGCGCGCGAGTCCGGAACCGCAGCAT 633

QY 346 ThrAspLysTyrPyrAsnPheMetLysGlnIleGlnArgAlaArgLysPheAsp 365
DB 634 CCGCAGCGGCTGCTGCTGCTGCGCGCGCTGCTGCTGCTGCGAGCAGTTTACGAG 693

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QY 366 GluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrpProValLeuThrAla 385
DB 694 GCCAGCAGCAGGACATCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGAGACGCGC 753

QY 386 LeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsnAsnPheThr 405
DB 754 CGCTGCTCATCGCGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 813

QY 406 ArgArgAlaTyrValSerLysProLysLysLeu-----LeuThr 418
DB 814 GCCCGCATCGCGCAGACAGCGCGCGCAGACCTCGCGCGCGCGCGCGCGCGCGCGCG 873

QY 419 LeuProIleAlaTyrAlaLysSerLeuValProPro-----AsnArgThrSerSer 435
DB 874 CTGATCTCACCGCGCACCTGCGTTAAGTGTCCCGCGCGCAGACAACTCTGAGACCGCG 933

QY 436 ProLeuAlaLys 439
DB 934 CCGAAGCGCGCG 945

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Search completed: January 16, 2004, 13:19:13
 Job time : 11694 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 16, 2004, 05:38:11 ; Search time 2815 Seconds
(without alignments)
3798.923 Million cell updates/sec

Title: US-09-847-081b-2
Perfect score: 2270
Sequence: 1 MSMSVALIMVVSPTSEVNSG.....IYAKSLVPPNRTSSPLAKT 440

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2.1/USPTO_spool/US09847081/runat.15012004.154337.1867/app.query.fasta.1.583
-DB=EST -QFMT=fastap -SUFIX=est -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi -LIST=45
-LOCALALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09847081.@CNCN 1.1.2810 @runat.15012004.154337.1867 -NCPU=6 -ICPU=3
-NO MAP -LARGEBUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

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2:	em_esthum:*
3:	em_estin:*
4:	em_estmu:*
5:	em_estov:*
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8:	em_hic:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_hic:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pln:*
20:	em_gss_vrt:*
21:	em_gss_fun:*
22:	em_gss_mam:*
23:	em_gss_mus:*
24:	em_gss_pro:*
25:	em_gss_rtd:*
26:	em_gss_png:*
27:	em_gss_vr1:*
28:	gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1214.5	53.5	819	13	B0636463
2	1211	53.3	1655	11	AY111032
3	1202	53.0	787	12	BM410846
4	1201.5	52.9	1201	11	AY108547
5	1179	51.9	781	13	B0511016
6	1136	50.0	751	12	B0046203
7	1130	49.8	765	12	BM408984
8	1099	48.4	686	9	AM442101
9	1083	47.7	682	12	BM409200
10	1072	47.2	672	9	AM442407
11	1049	46.2	642	10	BE433198
12	1043	45.9	676	9	AM222027
13	1001	44.1	677	10	BG515357
14	997	43.9	634	12	BM412533
15	984	43.3	704	14	CA999095
16	980	43.2	600	10	BE460889
17	977.5	43.1	623	10	BE432511
18	956	42.1	685	9	AM221932
19	947	41.7	581	9	AM223316
20	940	41.4	623	10	BE432955
21	939	41.4	623	12	BM536249
22	934	41.1	582	9	AM223666
23	927	40.8	605	10	BE435064
24	927	40.8	744	12	BM412719
25	921	40.6	562	10	BE433966
26	918	40.4	634	12	BM137086
27	917	40.4	565	10	BE432595
28	916	40.4	573	10	BE435308
29	915	40.3	881	14	CB621108
30	913	40.2	585	9	AM222245
31	907	40.0	668	12	B1955682
32	905	39.9	869	14	CB622557
33	899	39.6	556	9	AM222152
34	897	39.5	609	10	BE322877
35	891	39.3	581	9	AM222806
36	889	39.2	690	14	CB342702
37	884	38.9	791	9	AM223528
38	884	38.9	791	9	AM223528
39	881	38.8	542	10	BE431550
40	879	38.7	613	12	B1957464
41	877	38.6	543	12	BM411875
42	873	38.5	634	9	AM441216
43	873	38.5	687	10	BE434578
44	870	38.3	542	10	BE432748
45	869	38.3	888	14	CB621110

ALIGNMENTS

RESULT 1
B0636463
LOCUS B0636463
DEFINITION B0636463
ACCESSION B0636463
VERSION B0636463
KEYWORDS B0636463.1 GI:23303718
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroside II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 819)
 Lundsgerd, M., Emmersen, J., Nielsen, K.L., Wilson, I., Somerville, S.
 AUTHORS
 TITLE EST sequencing of *Erysiphe cichoracearum* infected *Arabidopsis*
 plants
 JOURNAL Unpublished
 COMMENT Contact: Karen G. Welinder
 Institut for bioteknologi
 Aalborg Universitet
 Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
 Tel: +45 96358467
 Fax: +45 98141808
 Email: kgw@bio.auc.dk.

FEATURES
 source 1..819
 Location/Qualifiers
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /dev_stage="Plant 3 weeks old, three days post infection"
 /clone_lib="Infected Arabidopsis leaf"
 /note="Organ: leaf; Vector: pBluescript; Mixed cDNA
 library of Arabidopsis and E. cichoracearum infected leaf
 from three weeks old Arabidopsis plants. Plants were
 harvested 3 days after infection and mRNA oligo dt
 selected."

BASE COUNT 245 a 158 c 205 g 211 t
 ORIGIN

Alignment Scores:
 Pred. No.: 5.78e-130 Length: 819
 Score: 1214.50 Matches: 220
 Percent Similarity: 92.99% Conservative: 22
 Best Local Similarity: 84.87% Mismatches: 16
 Query Match: 53.50% Indels: 3
 DB: 13 Gaps: 1

US-09-847-081b-2 (1-440) x BU636463 (1-819)

OY 165 ThrTysLeuMetThrProGluValArgArgAlaIleTTPAlaIleTTPValTTPCyArg 184
 Db 2 ACTTGTCTTATGACCCGGAAGGGGAAAGCGATTGGCAATCTACGTTGGTGGA 61
 OY 185 ArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGluAlaLeuAsp 204
 Db 62 AGAAGCTGATGAAGCTTGTGATGGCCAAATGCTTACATATACCTCCATGGCTTAAAT 121
 OY 205 ArgTTPGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeuAspAla 224
 Db 122 AGATGGGAAGCAAGCTTAGAAGATCTTTCCGTGGTCCCTTCGATATGCTGATGCT 181
 OY 225 AlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAspMetIle 244
 Db 182 GCTTCGGTGAACAGTGTAGATACCCGGTCGATATTCAGCCATTCGAGACATGATC 241
 OY 245 GluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeuTyrIleu 264
 Db 242 GAAGGAATGAGAAATGACTTGAAGAAATCGAGATCCGAAGCTTGAATGATCTATACCTT 301
 OY 265 TyrCyTrpTyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyTleAla 284
 Db 302 TACGTCTACTACGTGGTGAACCGTCGATGATGACGTTCCGTTATATGGAAATCAT 361
 OY 285 ProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAla 304
 Db 362 CCTATGTGAAGCAACCAACCGAAAGTGTTCACCAAGCTTCCTTGGCCCTTGTATACCC 421
 OY 305 AsnGluLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArgValTyr 324
 Db 422 AATCAGCTTACTACATCTACGAGACGTTAGCGAAGATGCGAAGAGGAAAGGGGTTAT 481
 OY 325 LeuProGluAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGlyArg 344
 |||||

Db 482 CTGCCTCAGATGAATTGGCTCAGGCTGGTCTTTTCAGATGAAGACATATTCGCCGAAAA 541
 OY 345 ValThrAspLysTrpArgAsnPheMetLysGlyGlnIleGlnArgAlaArgLysPhePhe 364
 Db 542 GTAAGCTGATATATGAGAAATCTTATGAAATGAGCTTAAACAGCAAGAAATTTCTTC 601
 OY 365 AspGluSerGluGlyValThrGluLeuAspSerAlaSerArgTTPProValLeuThr 384
 Db 602 GACCAAGCTGAGAAAGCGTCCAGCAAGCTCAGTCCGCTAGCAGATGGCCTGTATGGGCT 661
 OY 385 AlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGlnAlaAsnAspTyrAsnAspPhe 404
 Db 662 TCATTGGCTATTGTACAGAGATATCTGACGAGATTGAAGGAATGTACAAACAATTTT 721
 OY 405 ThrArgArgAlaTyrValSerLysPheLysLeuLeuThrLeuProIleAlaTyrAla 424
 Db 722 ACTAAGAGAGCTTATGTGGGAAAGTCAAGAAATTCAGCTTGCATTTGGCTTATGCT 781
 OY 425 LysSerLeuValProProAsnArgThrSerSer 435
 Db 782 AATCAGTACTA-----AAGACTTCAAGT 805

RESULT 2
 AV111032
 LOCUS
 DEFINITION Zea mays CL1906_1 mRNA sequence.
 ACCESSION AV111032
 VERSION AV111032.1 GI:21215622
 KEYWORDS
 HTG.
 SOURCE
 ORGANISM
 Zea mays
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1655)
 Hainey, C.F., Dolan, M., Mao, G.H., Vogel, J.M., Whitesitt, M.S.,
 Arthur, L.W., Hanafey, M., Morgante, M., and Tingey, S.V.
 Maize Mapping Project/Dupont Consensus Sequences for Design of
 Overgo Probes
 Unpublished (2002)
 2 (bases 1 to 1655)
 Coe, E.H.
 Direct Submission
 Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 If you are interested in getting corresponding physical clones,
 these are publicly available from ZmDB and may be found by BLAST
 searching at MSU, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.

FEATURES
 source 1..1655
 Location/Qualifiers
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="taxon:4577"
 /db_xref="taxon:4577"
 /clone_lib="Maize Mapping Project/Dupont Consensus
 Library"
 /note="this sequence is part of a project of EST
 assemblies resulting from the application of public
 contigs to seed Dupont contigs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project"

BASE COUNT 384 a 334 c 380 g 295 t 262 others
 ORIGIN

Alignment Scores:
 Pred. No.: 4.23e-129 Length: 1655
 Score: 1211.00 Matches: 244
 Percent Similarity: 79.47% Conservative: 27

Best Local Similarity:	71.55%	Mismatches:	66
Query Match:	53.35%	Indels:	4
DB:	11	Gaps:	3

QY	91	LeuValAlaSerProAlaGlyGluMetThrValSerSerGlyValbValTyrAspVal	110
Db	206	CTGCCCGTCMAACCCGGCGGAGAGGCCGCTGCTGTCTCCGACAGAAAGTCTACGACGTC	265
QY	111	ValLeuValbGlnAlaAlaLeuValbValbArgGlnLeuArgSerThrAspAspLeuGlnVal	130
Db	266	GTCGCTCAAGCAGGCGCGCATTCCTCAAAAGCCAGCTGCCG---ACGCGGCTCTCGACGCC	322
QY	131	LybPro---AspIleValbProGlybMetLeuGlyLeuLeuSerGlnAlaTyrAspArg	149
Db	323	AGGCCCCAGGACATGAGCATGCGACGCGAAC-----GGGCTCAAGAAAGCCTCAGCANNNN	376
QY	150	CysGlyGlnValbCysAlaGlyTyrAlaTyrThrPheTyrLeuGlyThrThyLeuMetThr	169
Db	377	NN	436
QY	170	ProGlybArgbArgbAlaIleTyrAlaIleTyrValTyrCysArgArgThrAspGlnLeu	189
Db	437	GAGGAGCGCGCGCGCGCATATGGCGCATTCATATGTGTGTAGAGGAGACATGACGCTT	496
QY	190	ValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTyrGlnThrArg	209
Db	497	GTAAGATGGGCGAAAGCCCACTACTATACACCAACAGCTTTGGACCGGATGGAGAAAGGA	556
QY	210	LeuGlnAspIlePheSerGlyArgProPheAspMetLeuAspAlaAlaLeuSerAspThr	229
Db	557	CTTAGAGATCTGTTTACCGGACGCTCTTACGACATGCTGATCCGCGCTCTCTGATATCC	616
QY	230	ValSerArgPheProValAspIleGlnProPheArgAspMetIleGlyMetArgMet	249
Db	617	ATCTCAAGSTTCCCATGACATTCAGCATTCAGGAGCATGATTGAAGGATGAGGAGT	676
QY	250	AspLeuTyrPheSerArgTyrIleThrPheAspGlyLeuTyrIleTyrCysTyrTyrVal	269
Db	677	GATCTTAGGAAGACAGAGTATTAACAATTCCAGCGAGCTCTACATGATCTACTGCTACTATTT	736
QY	270	AlaGlyThrValbGlyLeuMetSerValProValMetGlyIleAlaProGlySerIleVala	289
Db	737	GCTGGAACTGTCGGTATTAGACGTACTCTGTGATGGGCAATGCCAACCGAGCTTAACGA	796
QY	290	ThrThrGlySerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsn	309
Db	797	ACAACGTGAACCGTATACAGTACGTGCTCTGGATCGGAAATGTGCACCACTCACGAAAC	856
QY	310	IleLeuArgbAspValbGlyLeuAspAlaArgArgGlyValbTyrLeuProGlyAspGln	329
Db	857	ATTACTCGGGATGTTTGGAGAGATGCTTGAAAGAGAAAGATATATTACACACAAATAG	916
QY	330	LeuAlaGlnAlaGlyLeuSerAspGlnAspIlePheAlaGlyArgValThrAspLysTrp	349
Db	917	CTTGACACGAGCAGGGCTCTCTGATGAGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	976
QY	350	ArgAsnPheMetLysbGlnIleGlnArgAlaArgLysPhePheAspGlySerGlyLys	369
Db	977	NN	1036
QY	370	GlyValbThrGlnLeuAspSerAlaSerArgTyrProValbLeuThrAlaLeuLeuMetThr	389
Db	1037	GGGGTAATAGACTCTCACAGGCTTACGAGATGGCCAGTATGGGCTTCCCTGTGTTGTAC	1096
QY	390	ArgLysIleLeuAspGlnIleGlnAlaAsnAspTyrAsnAsnPheThrArgArgAlaTyr	409
Db	1097	AGCGACATCTCGAGATCGAAGCAACCAACGACTACCAACTTCACGAAAGGGCGTAT	1156
QY	410	ValSerLysProLysbLeuLeuThrLeuProIleAlaTyrAlaLysSerLeuValPro	429
Db	1157	GTTGGTAAGGAAAGATGTGTGACACTTCTCTGTGGCATATGAAAAATCGTATGCTC	1216

QY	430	PRO	430
Db	1217	CCA	1219

RESULT 3	LOCUS	DEFINITION	ACCSSION	VERSION	KEYWORDS	SOURCE	ORGANISM
BM410846	787 bp	EST58173 tomato breaker fruit Lycopersicon esculentum cDNA clone CLEG54F18 5' end, mRNA sequence.	BM410846	BM410846	GI:18262476	EST.	Lycopersicon esculentum (tomato)
							Lycopersicon esculentum

BASE COUNT	230 a	132 c	211 g	214 c
ORIGIN				

Alignment Scores:	
Pred. No.:	1.53e-128
Score:	1207.00
Percent Similarity:	95.00%
Best Local Similarity:	86.08%
Query Match:	52.95%
DB:	12
	0
Length:	78
Matches:	220
Conservative:	18
Mismatches:	13
Indels:	0
Gaps:	0

US-09-847-081B-2 (1-440) x BM410846 (1-787)

Oy 85 PhbSerValGIInSerSerIeuValAlaSerProAlaGIgIuMeTrnValSerSerGIu 104

Db 7 TTTTCCTGATCGGCTGCTATTTTGGCTACTCCATCTGGAGAACGACATATCACTCGAA 66

Oy 105 LysIleValTyrAspValValIeuIuysGlnAlaIleValLysArgIleLeuArgSer 124

Db 67 CAAATGGTCTATCAATGTGTTTGAACGACAGCGCTTGGTGAAGAGCAACTGAGATCT 126

Oy 125 ThrAspAspLeuGIuValLysProAspIleValProGIuAsnLeuGIuLeuLeuSer 144

Db	127	ACCAATGATGTAGAAGTGAAGCCGATPACTACTATTCGCGGGAAATTGGGCTGTGTTAGT	186
Qy	145	GLUALATYAAPAPhAqCyGgYglUuValCyalsagUtyrAlaYstH-PheTyrlengUy	164
Db	187	GAAGCATGTATGATGTGTGTGAGTATGATGTGTGAGATGTGTGAGATGTGTGAGAT	246
Qy	165	ThyrlsleuMeatThProGUuAqrgArgrAlaIleTpaIalleTyValTProCyArq	184
Db	247	ACTATGCTAAATGACTCCCGAGAGAAAGGGCTATCTGGGCAATATATGATGTGGCAGA	306
Qy	185	ArgThraePglUleuValaSPolProAnaIaseRhlSileThProGUuAlaUleuASP	204
Db	307	AGAACAGATGAACCTTGTGATGCGCCCAACGATCATATATTACC CGGACCTTAAAT	366
Qy	205	ArgTPrGUthraUrgLeuGUuAspIlePheSerGlyArqProPheASPmetUleuAspAla	224
Db	367	AGGTGGGAAATAGCGCTGAAGATCTTTTCATATGAGCGCGCATTTGACATGCTCATGT	426
Qy	225	AlaIeusArAPThValSerArqPheProValaSPllEgInProPhaUASPmetIle	244
Db	427	GCTTGTCCGATACGCTTCTTAACCTTCAGTGTATTCAGCCATTCAGAGATATGATT	486
Qy	245	GUglUyMeCArgMeCAspLeuTPrlySseArqTyrlYstHrPhaASPglUleuTyrlUeu	264
Db	487	GAAGAAATGCCGATGTGACTGTGAGAAATTCGAGATATCAAAAACCTTGACAGACTATACCTT	546
Qy	265	TyrCyStyTyTyValAlaGlyThrValGlyUeuMeTserValProValMeCtylLeaIa	284
Db	547	TATGTGTATTTATGTGCTGTGTGATCGGCTTGATGAGATGTTCATATATGATGTATCCGC	606
Qy	285	ProGUserUyAlaThThrGUserValTyraAnaIaAlaUleuGlyUleuAla	304
Db	607	CCTGATCAAAAGGCAACACAGAGCGCATATATATGCTTGCTTGCGGATGCCA	666
Qy	305	AsnGUleuThraSnIleUeuArqSPValGlyGUuAspAlaArqArGlyArqValTyrl	324
Db	667	AATCATTTAATCTAATCACTACTCAGAGATGTGGAGAAAGATCCAGAAAGAAAGATCTAC	726
Qy	325	LeuProGUuAspGUleuAlaGUuAlaGlyUeuSerAspGUuAspIlePheAlaGlyArq	344
Db	727	TTGCGCTCAGATGATATGACACAGCGAGGTCTATCCGATGAAGATATATTTGCTCGAAG	786
RESULT 4			
LOCUS	AY108547	1201 bp	mRNA
DEFINITION	Zea mays	PCO131047	mRNA sequence.
ACCESSION	AY108547		
VERSION	AY108547.1	GI:21211629	
KEYWORDS	HTC.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD		
TITLE	clade; Panicoideae; Andropogoneae; Zea.		
	1 (bases 1 to 1201)		
	Unpublished (2002)		
JOURNAL	2 (bases 1 to 1201)		
REFERENCE	Coe, E.H.		
TITLE	Direct Submission		
AUTHORS	Submitted (25-APR-2002)		
JOURNAL	Missouri, Columbia, MO 65211, USA		
COMMENT	Maize Mapping Project, University of		
	If you are interested in getting corresponding physical clones,		
	these are publicly available from ZmDb and may be found by BLAST		
	searching at MSU, maizemap.org ; ZmDb, www.zmdb.iastate.edu ; TIGR,		
	www.tigr.org ; or NCBI, www.ncbi.nlm.nih.gov . When the source of the		
	maize cDNA sequences is either Virginia Walbot, Stanford or Pat		
	Schnable, Iowa State, then clones may be requested from ZmDb:		
	www.zmdb.iastate.edu .		
FEATURES	Location/Qualifiers		

Source	1. 1201	273 a	325 c	316 g	287 t
source	1. 1201				
	/organism="Zea mays"				
	/mol_type="mRNA"				
	/db_xref="MaizeDB:637648"				
	/db_xref="taxon:4577"				
	/clone_lib="Maize Mapping Project/Dupont Cornsensus library"				
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"				
BASE COUNT	273 a	325 c	316 g	287 t	
ORIGIN					
Alignment Scores:					
Pred. No.:	3.3e-128	Length:	1201		
Score:	1201.50	Matches:	223		
Percent Similarity:	92.62%	Conservative:	28		
Best Local Similarity:	82.29%	Mismatch:	19		
Query Match:	52.93%	Indels:	1		
DB:	11	Gaps:	1		
US-09-847-081B-2 (1-440) x AY108547 (1-1201)					
QY	161 PheTYrIleu--GlyThrLyLeuWetThrProGIuATgATgATgAlaIleTPaIle	179			
DB	167 TTTTACGCTTACAGGCGACGACCTCATGACTCTCGAGCGCCCAAGCGCTGGCGCATC	226			
QY	180 TyrValTTCyAArgArgThrAspGIuLeuValAspGIyProAnaIAserHisIleThr	199			
DB	227 TACGTGGGGAGAAAGAACTAGAGAGGTCTCCCAAGCGGTCTTACATACG	286			
QY	200 ProGIAlaLeuAspArgTrpGIuThrArgLeuGIuAspIlePheSerGIyArgProPhe	219			
DB	287 CCGACCGCTCTGCACCGCGTGGAGAGCGCGTGGAGATCTCTTGAAGGCGCGCGTAC	346			
QY	220 AspMetLeuAspAlaIaLeuSerAspThrValSerArgPheProValAspIleGIuPro	239			
DB	347 GACATGACGACGCGCGCTCTGCAGACTGTGTCAAGTTCCCGCTCATACACCG	406			
QY	240 PheArgAspMetIleGIuIleMetArgMetAspLeuTrpIlySerArgTrpLyThrPhe	259			
DB	407 TTCAAGACATGTGTCCAAAGAAATGAGCGCTGCAGCTGTGAAGTCAAGATATGACCTTC	466			
QY	260 AspGIuLeuTYrIleuTYrCySTyrTYrValAlaGIyThrValGIyLeuMetSerValPro	279			
DB	467 GACGAGCTTACTCTCTACTGCTACTACGTCCGCGGACCGCTCGGCTCATGACGCTGCT	526			
QY	280 ValMetGIyIleAlaProGIuSerIlyAspIleThrThrGIuSerValTYrAspAlaIleu	299			
DB	527 GTCATGGGATGCTCGCGATCCCAAGGCGTGCAGCGAGCGGTCAATGCTGCTCTG	586			
QY	300 AlaLeuGIyLeuAlaAsnGIuLeuThrAsnIleLeuArgAspValGIyGIuAspAlaArg	319			
DB	587 GCTCTCGGATCTGCTTACAGCTGACGAATATCTTCAAGACGCGGCGAAGAGCGAGG	646			
QY	320 ArgGIyArgValTYrIleuProGIuAspGIuLeuAlaGIuIleAspIleLeuSerAspAlaAsp	339			
DB	647 AGGGGAGAAATATACCTTCTGTTGACAGACGCTTGGCGAGCGGTCTTACGAGAGAGAC	706			
QY	340 IlePheAlaGIyArgValThrAspIlySTrPArgAspMetIlySlyGIuIleGIuArg	355			
DB	707 ATATTCAGAGGAAAGTGAACGCAAGTGAAGAGATTCATGAAGGGCAGATCCACGCT	766			
QY	360 AlaArgIlyPhePheAspGIuSerGIyIlyValThrGIuLeuAspSerAlaSerArg	379			
DB	767 GCCAGGCTCTTCTTATGAGCGCGAGAGAGGCGTCAACCTTCGACTGTGTGACGA	826			
QY	380 TrpProValIleuThrAlaLeuLeuLeuTYrArgIlyIleLeuAspGIuIleGIuAlaAsn	399			
DB	827 TGGCCGATGCTCCGCTCTGTGGCTGTACAGCGAGATCTTGAATGCCATTGAGGAAAC	886			

QY 400 APTTYAAsnAsnphethrArgrAlaTyValSerlyeProlyleyleuLeuThleu 419
|||||
Db 887 GACTACAAACACTTCACCAAGCGTGCTAGTCGAGCAAGAGAGCTGCTGTCTTA 946
QY 420 ProtleAlATYrAlAlalysSerleuValProPro 430
|||||
Db 947 CCGCTTGACATATGCAAGGCTGCTGTGACCA 979

RESULT 5
BOS11016/c

LOCUS
DEFINITION
BOS11016 781 bp mRNA linear EST 07-MAR-2003
EST18431 Generation of a set of potato CDNA clones for microarray
analyses mixed potato tissues Solanum tuberosum CDNA clone SYMH067
3' end, mRNA sequence.

ACCESSION
BOS11016 GI:21926690
VERSION
BOS11016.2 GI:21926690
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 781)
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
Karamycheva, S.A.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished
On Jun 10, 2002 this sequence version replaced gi:21369885.
Other ESTs: EST618430
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T7.

FEATURES
source
Location/Qualifiers
1..781
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec or Binje"
/db_xref="taxon:4113"
/clone="STMH067"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/clone_lib="Generation of a set of potato CDNA clones for
microarray analyses mixed potato tissues"
/note="Vector: pBluescript SK(-), Site 1: EcoRI, Site 2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
tubers, or roots."

BASE COUNT 202 a 191 c 144 g 244 t
ORIGIN

Alignment Scores:
Pred. No.: 7.04e-126 Length: 781
Score: 1179.00 Matches: 230
Percent Similarity: 96.36% Conservative: 9
Best Local Similarity: 93.12% Mismatches: 8
Query Match: 51.94% Indels: 1
Dg: 13 Gaps: 0

US-09-847-081b-2 (1-440) x BOS11016 (1-781)

QY 194 AenAlaserHisIlePhProGlnAlaLeuAspArgTrpGluThrArgIleuAspIle 213
|||||
Db 781 AATGATCAACATTAATCAACAGCTTAGATAGGCTGGAGCCAGGCTGGAAGATAT- 723
PheSerGlyArgProPheAspMetLeuAspAlaIleuSerAspThrValSerArgPhe 233

Db 722 TTCACAGGGCGGCCATTGATATGCTTATGAGCTTATCCGATATCGTTCCAAATTT 663
QY 234 ProValAspIleIleGlnProPheArgAspMetIleGluGlyMetArgMetAspLeuTrpLys 253
Db 662 CCGTGTGATATTCACCATTCAGATATGATGTAAGAAATCCGATGATCTGTGGAAA 603
QY 254 SerArgTyLeuThrPheAspGluLeuTyLeuTyLeuTyLeuTyLeuVal 273
Db 602 TCCAGATACACAACTTGATGATGATATATCTATATGTTACTTATGCTGCTGACAGTA 543
QY 274 GlyLeuMetSerValProValMetGlyIleAlaProGluSerIleAlaThrGluSer 293
Db 542 GGATTGATGAGAGTTCATTATATGAGCTTGGCACTGCAATCAAGGCAACAGAGAGAT 483
QY 294 ValTyAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAsp 313
Db 482 GTATATTAACGCGCTTGGCTTACGAGATCGCAAAATCACTAACCAATATCTCAGAGAT 423
QY 314 ValGlyGluAspAlaArgArgGlyArgValTyLeuProGlnAspGluLeuAlaIle 333
Db 422 GTAGAGAAAGATGCAAGAAAGAGATATCTTACCTCAAGATGATTAACACAGGCA 363
QY 334 GlyLeuSerAspGluAspIlePheAlaGlyArgValThrAspIleTyArgAspMet 353
Db 362 GGGCTCTCCGATGAAAGACATTTTCTGGAAGAGTACGATATAGTGGAGATCTTTATG 303
QY 354 LysLysGlnIleGlnArgAlaArgLysPhePheAspGluSerGlyValThrGlu 373
Db 302 AAGAAAGCAAAATTCACAGGGCAAGAAATCTTGTAGAGGCGAAAGTGTACAGAA 243
QY 374 LeuAspSerAlaSerArgTrpProValLeuThrAlaLeuLeuTyArgLysIleLeu 393
Db 242 CTGACCTCTGCTAGTAGAATGGCGGTGTGGCTGTGCTATATGCAAGATACG 183
QY 394 AspGluIleGluAlaAsnAspTyAsnAsnphethrArgrAlaTyValSerLysPro 413
Db 192 GACGAGATTGAAGCAAGCAAGATACCAACTCACAGAGAGGCTTATGTAGCAAGCA 123
QY 414 LysLysLeuLeuThrLeuProIleAlaTyAlaLysSerLeuValProProAsnArgThr 433
Db 122 AAGAGCTTCTGACCTTCCCATTCCTTATGACAGATCTCTAGTCCCTTAATCAACT 63
QY 434 SerSerProLeuAlaLysThr 440
Db 62 TCTTCCCACTAGCAAGACA 42

RESULT 6
B0046203

LOCUS
DEFINITION
EST595321 P. infestans-challenged potato leaf, incompatible
reaction Solanum tuberosum CDNA clone BPL14E21 5' end, mRNA
sequence.

ACCESSION
B0046203
VERSION
B0046203.1 GI:19820189
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 751)
Zhang, P., Hernandez, M., Tornqvist, C.-E., Wirtz, U., Loukoianov, A.,
Rangel, P., Haberer, G.T., Karamycheva, S.A., Tsai, J., Chienlingo, A.,
Bougril, O., Buell, C.R., Roming, C.M., Helgeson, J. and Baker, B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora
infestans, incompatible interaction (2002)
Unpublished

TITLE
JOURNAL
COMMENT
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
This clone can be obtained from the University of Arizona Genomics

Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3.

FEATURES
SOURCE Location/Qualifiers

```
1..751
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="BPL114E21"
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
/clone_lib="P. infestans-challenged potato leaf,
incompatible reaction"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: UC Berkeley, PGSC; sequencing: The
Institute for Genomic Research. Whole plants were
challenged with 450,000 sporangia/ml P. infestans isolate
US-1 (US940501) in Biotron (Madison, Wisconsin). Leaf
tissue was collected at 1, 2, 5, 12, and 24 hours
post-challenge and frozen in liquid nitrogen immediately
upon removal. Kennebec plants showed no signs of HR.
Katahdin plants (susceptible to P. infestans US-1) were
used as controls and showed infection. NOTE: We cannot
exclude the possibility that this sequence is actually
derived from Phytophthora rather than potato."
```

BASE COUNT 219 a 119 c 199 g 214 t

ORIGIN

Alignment Scores:

```
Pred. No.: 6,44e-121 Length: 751
Score: 1136.00 Matches: 225
Percent Similarity: 94.40% Conservative: 11
Best Local Similarity: 90.00% Mismatches: 12
Query Match: 50.04% Indels: 3
DB: Gaps: 0
```

US-09-847-081b-2 (1-440) x BQ046203 (1-751)

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QY 67 AAlaAPPpRoAgtTgTtSerCyLeuGlySerAgtThrGluValSerThrPheSer 86
Db 5 GCAGATTGAGATATTCGTGTTAGGAAGATCAAACTGGAAGAAAGAGAGGCTTTTCT 64
QY 87 ValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSerSerGluValys 106
Db 65 GTACAGTCCAGTTTGTTGGCTAGTCCAGCTGAGAAATGGCTGTCTATCGAGAAAAAG 124
QY 107 ValTyRAspValAlaLeuLysGlnAlaAlaLeuValLysArgGlnLeuArgSerThrAsp 126
Db 125 GTGATATGAGGTGATTTGAGAGAGCAGCTTTAGTGAAGAGCAGCTATATCTACTGAG 184
QY 127 AspleuGluValLysProAspLLeValAlaProGlyAsnLeuGlyLeuLeuSerGluAla 146
Db 185 GACATAGAGAGAACCCGATATTTGTTCCGGCTAATTTGGGCTTTGAGTGAACGA 244
QY 147 TyrAspArgCyGlyGluValCysAlaGluTyrAlaLysThrPheTyrLeuGlyTThrLys 166
Db 245 TATGATTCGTGTGGGAGAGATATGCAAGATGCTAAAGACATTTACTTGAAGACCAATG 304
QY 167 LeuMetThrProGluArgArgAlaIleTrrAlaIleTrrValTrrCysArgArgThr 186
Db 305 CTAATGACTCCAGACAGAAAGAGACTATCTGGCAATATATGTGTGGTGGAGGAACT 364
QY 187 AspleuLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTrr 206
Db 365 GATGAGCTTGTGTGATGGCCCTAATCATCACACATCACTCCCAAGCTTTGATAGTGG 424
QY 207 GluThrArgLeuGluAspLLePheSerGlyArgPProPheAspMetLeuAspAlaLeu 226
Db 425 GAGGCGAGGCTGGAGATATTTTCAACGGGCGGCTTTGATATCTCTTGAAGACCTTTA 484
QY 227 SerAspThrValSerArgPheProValAspLLeGlnProPheArgAspMetLLeGluGly 246
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Db 485 TCCATATCTGTTTCCAAATTCCTGTTGATATTCAGCCATTCAGAGATATGTTGAAGA 544
QY 247 MetArgMetAspLeuThrPlysSerArgTyrLysThrPheAspGluLeuTyrLeuTyrCys 266
Db 545 ATGGGATGGAGCTGTGGAAATCCAGATACCAACACTTTGATGAACTATATCTATTTGT 604
QY 267 TyrTyRValAlaGlyThrValGly-LeuMetSerValProValMetGlyIleAlaProGly 286
Db 605 TACTATGTCGTGTATAGTAGAATGATGAGAGTTCATATATATGAGCAATTCAGCCTGA 664
QY 286 USeTyRAlaThrThrGluSerValTyrAsnAlaAla-LeuAlaLeuGlyLeuAlaAsnG 306
Db 665 ATCCAGAGCAACGACAGAGAGTATATACGACGCTTTTGGCTTTGAGGATCCCAATC 724
QY 306 LLeuThrAsnLLeuArgAspVal 314
Db 725 AACTAACCAT-ATACTCAAGATGTA 749
```

RESULT 7
LOCUS BM408984 765 bp mRNA linear EST 22-JAN-2002
DEFINITION EST583311 tomato breaker fruit Lycopersicon esculentum cDNA clone
C1EG46P23 5' end, mRNA sequence.
ACCESSION BM408984
VERSION BM408984.1 GI:18260614
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum

REFERENCE
AUTHORS Alcala,J., Vrebalov,J., White,R., Vasion,T., Karamycheva,S.A., Tsai
,J., Bougri,O., Kikinesh,R., Uterback,T., Van Aken,S., Roming
,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished
CONTACT: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.

FEATURES
SOURCE Location/Qualifiers

```
1..765
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="C1EG46P23"
/tissue_type="Pericarp"
/dev_stage="Breaker"
/lab_host="SOLR"
/clone_lib="tomato breaker fruit"
/note="Vector: pBluescriptSKmudapt; Site_1: EcoRI;
Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
```

BASE COUNT 237 a 122 c 202 g 204 t

ORIGIN

Alignment Scores:

```
Pred. No.: 3.29e-120 Length: 765
Score: 1130.00 Matches: 222
Percent Similarity: 90.94% Conservative: 9
Best Local Similarity: 87.40% Mismatches: 20
Query Match: 49.78% Indels: 3
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DB: 12 Gaps: 2

US-09-847-081b-2 (1-440) x BM408384 (1-765)

QY 128 LeuGUValIysProaspIleValProGIYAsnLeuGIYleuLeuSerGIUAlaTYR 147

DB 1 TTAGAGAGTAAAGCCGGAATTAATCTATTCGGGGAAATTTGGGCTGTGTGAGTAAAGCATAT 60

QY 148 AspArgCysGlyGUValCysAlaGIUValAlaYsthrPheTYrLeuGIYThrlYsleu 167

DB 61 GATAGGTGTGTGAATATATGTGAGAGTATGCAAAACGTTTAACTTAGGAAGTATGCTTA 120

QY 168 MetThrProGIUArgArgAlaIleTYrPalalIeTYrValTYrCysArgArgThrasp 187

DB 121 ATGACTCCCGAGAGAGAGAGGCTATCTGGGCAATATATGTATGTGTGAGAGAAACAGAT 180

QY 188 GluLeuValAspGIYProAsnAlaSerHisIleThrProGIUAlaLeuAspArgTTPGIU 207

DB 181 GAACCTGTGTGATGGCCCAACGATCATATATTAATCCCGCACCTTAGATAGTGGGAA 240

QY 208 ThrArgLeuGIUAspIlePheSerGIYArgProPheAspMetLeuAspAlaIleAsnSer 227

DB 241 AATAGGCTTGAAGATCTTTCAATGGGCGGCCATTTGACATGCTCGATGCTTGTCTCC 300

QY 228 AspThrValSerArgPheProValAspIleGIUProPheArgAspMetIleGIUArgMet 247

DB 301 GATACAGTTTCTTAACCTTCCAGTTGATATTCAGCCATTCAGAGATATGATTTGAGAGATG 360

QY 248 ArgMetAspLeuTrpIysSerArgTYrLYsthrPheAspGIULeuTYrLeuTYrCysTYR 267

DB 361 CGTATGGACTTGAGAAATCGAGATCAAAAACCTTCGACAGACTATACCTTTATTTCTTAT 420

QY 268 TYrValAlaGIYThrValGIYleuMetSerValProValMetGIYIleAlaProGIUUser 287

DB 421 TATGTTCGTCGTACGGTTGGTTGATGAGTGTTCATTTATGGATATCGCCCTGATACA 480

QY 288 LysAlaThrThrGluSerValTYrAsnAlaIleAlaLeuAlaLeuGIYleuAlaAsnGIUleu 307

DB 481 AAGGCACACACAGAGAGCGTATATATATGCTTGGCTTGGGAGTCCCAATCAATTA 540

QY 308 ThrAsnIleLeuArgAspValGIYGUAspAlaArgArgGIYArgValTYrLeuProGIU 327

DB 541 ACTAACATTACTCAGAAATGTGGAGAAATGCCAGAGAGAGAAAGATCTTACTGCTCTCA 600

QY 328 AspGIUleuValAlaGIUAlaGIYleuSerAspGIUAspIle-PheAlaGIYArgValThrasp 347

DB 601 GATGATTTTACACAGGAGGCTCTATCCAGTAAAGATATTTTGGCTGGAGAGGCTGACCA 660

QY 347 PLYSTrPArgAsnPheMetIleYsleGIUleGIUArgAlaArgIYsPheAspGIUSe 367

DB 661 TTAATGGAGAAATCTTTATGAGAAACA---TACTAGGGCAGAAAGTCTTTGATGAGCA 717

QY 367 tGIUysGIYValThrGIUleuAspSerAlaSerArgTTP 380

DB 718 GAGAAAGCGT---GACAGATGAGCTCAGCTAGTATGATTC 754

RESULT 8
AM442101

LOCUS ESTJ11497 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA

DEFINITION clone cLENI2G20 5', mRNA sequence.

ACCESSION AM442101

VERSION AM442101.1 GI:6977352

KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 686)

Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Romming,C.M., Frazer,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.

TITLE Generation of ESTs from tomato fruit tissue

JOURNAL Unpublished

COMMENT Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

5 prime sequence.

FEATURES

source

1..686

location/Qualifiers

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/culivar="PA496"

/db_xref="taxon:4081"

/clone="cLENI2G20"

/tissue_type="pericarp"

/dev_stage="red ripe (7-20 days post-breaker)"

/clone_1ib="tomato fruit red ripe, TAMU"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Giovannoni; Fruit were tagged at the breaker stage (first sign of lycopen accumulation on the blossom end of the fruit) and harvested 7 days post-breaker (fully red-ripe), 10 days post breaker, and 20 days post-breaker (over-ripe). 20 day fruit which showed external or internal signs of pathogenesis were discarded. Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

BASE COUNT 204 a 114 c 182 g 186 t

ORIGIN

Alignment Scores:

Pred. No.: 1..1e-116 Length: 686

Score: 1099.00 Matches: 209

Percent Similarity: 95.61% Conservative: 9

Best Local Similarity: 91.67% Mismatches: 10

Query Match: 48.41% Indels: 0

DB: 9 Gaps: 0

US-09-847-081b-2 (1-440) x AM442101 (1-686)

QY 108 TYrAspValIleuLeuysGIUAlaIleuValIysArgGIUleuArgSerThrasp 127

DB 2 TATGATGTGTGTTTATGAGCAGGACCTTGTTGGAAGAGCACTGATCTACCATGAG 61

QY 128 LeuGIUValIysProaspIleValValProGIYAsnLeuGIYleuLeuSerGIUAlaTYR 147

DB 62 TTAGAGAGTAAAGCCGGAATATATCTTCCGGGAATTTGGGCTTGTGTGAGAACATAT 121

QY 148 AspArgCysGlyGUValCysAlaGIUValAlaYsthrPheTYrLeuGIYThrlYsleu 167

DB 122 GATAGGTGTGTGAAGTATGTGACAGATATGCAAAACGTTTAACTTAGGAAGTATGCTTA 181

QY 168 MetThrProGIUArgArgAlaIleTYrPalalIeTYrValTYrCysArgArgThrasp 187

DB 182 ATGACTCCCGAGAGAGAGGCTATCTGGGCAATATATGTATGTGTGAGAGAAACAGAT 241

QY 188 GluLeuValAspGIYProAsnAlaSerHisIleThrProGIUAlaLeuAspArgTTPGIU 207

DB 242 GAACCTGTGTGATGGCCCAACGATCATATATTAATCCCGCACCTTAGATAGTGGGAA 301

QY 208 ThrArgLeuGIUAspIlePheSerGIYArgProPheAspMetLeuAspAlaIleAsnSer 227

DB 302 AATAGGCTTGAAGATGTTTCAATGGGCGCCATTTGACATGCTCGATGCTTGTCTCC 361

QY 228 AspThrValSerArgPheProValAspIleGIUProPheArgAspMetIleGIUArgMet 247

DB 362 GATACAGTTTCTTAACCTTCCAGTTGATATTCAGCCATTCAGAGATATGATTTGAGAGATG 421

QY 248 ArgMetAspLeuTrpIysSerArgTYrLYsthrPheAspGIULeuTYrLeuTYrCysTYR 267

DB 422 CGTATGGACTTGAGAAATCGAGATCAAAAACCTTCGACAGACTATACCTTTATTTCTTAT 481

QY 268 TYrValAlaGIYThrValGIYleuMetSerValProValMetGIYIleAlaProGIUUser 287

Db	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	1482	TATGTCTGCTACCGCTTGGCTTATAGAGTGTCCAAATTATGAGTATGCCCCCTGAAATCA						
Qy	288	LysalathrhrngluserValTyrAsnAlaIaleuAlaIeuglYleuAlaAsnIleu						
Db	542	AAGCAACACAGAGAGCGTATATATGCTGCTTGGCTTGGGATGCAATCAATTA						
Qy	308	ThrAnlleleuAArgAspValGlyGluAspAlaAArgGlyArgValTyrIleuProGln						
Db	602	ACTACACATCTCCAGAGATGTGGAGAAATGCGACAGAGAGAGAGTCTACTTGCTCA						
Qy	328	AspGluLeuAlaGlnAlaGlyLeu						
Db	662	GATGATTTATACCCAGCAGTCTA						
RESULT 9								
BM409200								
LOCUS								
DEFINITION								
ACCESSION								
VERSION								
KEYWORDS								
SOURCE								
ORGANISM								
REFERENCE								
AUTHORS								
TITLE								
JOURNAL								
COMMENT								
FEATURES								
source								
Location/Qualifiers								
1..682								
/organism="Lycopersicon esculentum"								
/mol_type="mRNA"								
/cultivar="TA496"								
/db_xref="taxon:4081"								
/clone="CLG4701"								
/tissue_type="pericarp"								
/dev_stage="breaker"								
/lab_host="SOLR"								
/clone_11b="tomato breaker fruit"								
/note="Vector: pBluescriptSmCtadpt; Site 1: EcoRI; Site 2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopen accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."								
BASE COUNT								
ORIGIN								
Alignment Scores:								
Pred. No.:								
Score:								
Percent Similarity:								
Best Local Similarity:								
Query Match:								
Db:								

Qy	155	AlaGluIuYrAlaIysThrPheTyrlEuGIuThLysLeuMetThrProGluuAaGArGArg	174
Db	1	GCAAGATGATCAAGAAAGCTTAACTTAAGAACTATGCTTAATGACTCCGAGAGAAAGG	60
Qy	175	AlaIleTrpAlaIaIeTyValTrPCysArGArGThrAspGluLeuValAaSpGIyProAsn	194
Db	61	GCATATCGGGCAGATATATATGATGGTGCAGAAAGAACGATGAATTGTTGATGGCCAAAC	120
Qy	195	AlaSerHisIleThrProGluuAlaLeuAspArGTPrGluThrArgLeuGluAspIlePhe	214
Db	121	GCATCATATATTTACCCCGCAGCGCTTGATGATGGTGGGAAATAGGCTAGAAAGATGTTTTC	180
Qy	215	SeclIyArgProPheAspMetLeuAspAlaIaLeuSerAspThrValIserArgPhePro	234
Db	181	AATGGGGGGCCATTGACATGCTCGAAGGTGGCTTGTCCATACAGTTCTTAACCTTCCA	240
Qy	235	ValAspIleGluInProPheArGAspMetIleGluGIyMetArgMetAspLeuTrpLysSer	254
Db	241	GTTGATATTTACGCCATTACAGATATGATTTGAAGGAATGCGTATGCACTTGAGAAATCG	300
Qy	255	ArgTrIyLysThrPheAspGluLeuTyrlEuTyrlCysTrTyValAlaGlyThrValGIy	274
Db	301	AGATACAAAACCTTCGACGAACATATACCTTATTTGTTATTTATGTCGTGACGAGGGG	360
Qy	275	LeuMetSerValProValMetGIyIleAlaProGluSerIyAlaThrTrpGluSerVal	294
Db	361	TTGATGAGTGTTCCAATATGATGGATGATGCCCTCGAATCAAGGCACAAACGAGAGCGTA	420
Qy	295	TyrAsnAlaIaLeuAlaIeGluGIyLeuAlaAsnGIuLeuThrAsnIleLeuArGAspVal	314
Db	421	TATATATCTGCTTTGGCTCTGGGGATGCGAAATCAATTAATCAATCACTCAAGAGATGT	480
Qy	315	GIyGIuAspAlaArGArGGIyArGValTyrlEuProGluAspGluLeuAlaGluAlaGIy	334
Db	481	GGAGAAAGATGCCAGAAAGAGAGCTCTACTTGCCTCAAGATGAATATATCACAGGCGAGT	540
Qy	335	LeuSerAspGluAspIlePheAlaGIyArGValThrAspIyStrTPArgAsnPheMetLys	354
Db	541	CTATCCGATGAAGATATATTTGCTCGAAGAGGTGACCGATTAATGGAAGAATCTTATTAAG	600
Qy	355	LysGluIleGluInArGAlaArGIyPhePheAspGluSerGIuIySGIyValThrGIuLeu	374
Db	601	AAACAAATACCTAAGCGCAAGAACTTTTTCATGAGGCAAGAAAGCGCTGACAGATTTG	660
Qy	375	AspSerAlaSerArGTPrPro	381
Db	661	AGCTCAGCTAGTAGATTCCT	681
RESULT 10			
AM442407			
LOCUS		672 bp	mRNA
DEFINITION		EST311803 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA	
ACCESSION		clone GLEN22L14 5', mRNA sequence.	
VERSION		AM442407	
KEYWORDS		AM442407.1	GI:6977658
ORGANISM		EST.	
SOURCE		Lycopersicon esculentum (tomato)	
REFERENCE		Lycopersicon esculentum	
AUTHORS		Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; asterids; lamids; Solanales; Solanales; Solanales; Solanum; Lycopersicon.	
TITLE		1 (bases 1 to 672)	
JOURNAL		Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upson,J., Hansen,T., Craven,M.B., Bowman,C.L., Ann,S., Ronting,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.	
COMMENT		Generation of ESTs from tomato fruit tissue	
		Unpublished	
		Contact: CUGI	
		Clemson University Genomics Institute	
		Clemson University	
		100 Jordan Hall, Clemson, SC 29634, USA	
		Email: http://www.genome.clemson.edu/orders/index.html	
		5 prime sequence.	

SOURCE Solanum tuberosum (potato)

ORGANISM Solanum tuberosum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.

AUTHORS 1 (bases 1 to 677)

TITLE The potato tuber transcriptome: analysis of 6077 expressed sequence tags

JOURNAL FEBS Lett. 506 (2), 123-126 (2001)

MEDLINE 21475600

PUBMED 11591384

COMMENT Contact: Karen G. Wellinder
Instituit for biotecnologi
Aalborg Universitet
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel.: +45 96358467
Fax: +45 98141808
Email: kgy@bio.auc.dk
Sequenced from the 5' end.
High quality sequence stop: 677
POLYA=No.

FEATURES

source Location/Qualifiers

1..677

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Field grown Kuras"

/db_xref="taxon:4113"

/tissue_type="tuber"

/clone_lib="Mature tuber lambda ZAP"

/note="Vector: Lambda ZAP"

BASE COUNT 192 a 102 c 198 g 185 t

ORIGIN

Alignment Scores:

Pred. No.: 2.5e-105 Length: 677

Score: 1001.00 Matches: 195

Percent Similarity: 91.15% Conservative: 11

Best Local Similarity: 86.28% Mismatches: 20

Query Match: 44.10% Indels: 1

DB: 10 Gaps: 0

US-09-847-081b-2 (1-440) x BG351357 (1-677)

QY 25 AappserValaRgGlUGlYAsnaRgValPheValSerSerArgPheLeuAlaRgAspArg 44

Db 1 GATTGAGTCCGAGAGGGAACCGGG-TTGAATCATCCAGGTCCCATCTCCGATAGG 59

QY 45 AsnLeuMetTrpAsnGlyArgIleLysLysGlyArgGlnArgTrpAsnPhgGlySer 64

Db 60 AATTGAGTGTGGAAGGAGATTCAAGAAAGGTGGAGACAGAGTGGAAATTTGGGTTT 119

QY 65 LeuIleAlaAspProArgTrpSerCysLeuGlyGlySerArgThrGluLysGlySerThr 84

Db 120 TTAATGCAAGATTGATGATTCGTGTTAGCAAGATCAAGAACTGAGAAAGAGAGT 179

QY 85 PheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSerSerGlu 104

Db 180 TTTTGTGACATCCAGTTGTGGCTGAGTCCAGCTGGAAGATGCTGTGCATCAGAG 239

QY 105 LysLysValIYrAspValValLeuLysGlnAlaAlaLeuValIYrAspGlnLeuArgSer 124

Db 240 AAAAAGGTGTAGAGTGTATTGAAGCAGCAGCTTTAGTGAAGAGCATGTATATT 299

QY 125 ThrAspAspLeuGlnValIYrAspIleValIYrProGlyAsnLeuGlyLeuLeuSer 144

Db 300 ACTGAGCATGTAGAGTGAAGCCGATATTGTTGTCGCGTAATTGGGCTTGTAGT 359

QY 145 GluAlaIYrAspAspCysGlyGluValCysAlaGluIYrAlaIYrThrPheTrpLeuGly 164

Db 360 GAAAGCATATGATCGTGTGGCAGAGATGTGCAAGATGTCAAGCATTTTACTTAGGA 419

QY 165 ThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIleTrpValIYrPysArg 184

Db 420 ACCATGCTAATGACTCCAGACAGAAAGAGCTATCTGGCAATATATGTGGTGCAGG 479

QY 185 ArgTrpAspGluLeuValAspGlyProbenAlaSerHisIleThrProGlnAlaLeuAsp 204

Db 480 AGAAGCATGAGCTGTGTGATGGCCCTTAATGATACACATACCTCCAAACCTTAGAT 539

QY 205 ArgTrpGluThrArgLeuGlnAspIlePheSerGlyArgProPheAspMetLeuAspAla 224

Db 540 AGGTGGAGGCCAGCTCGAAGATATTTTCAACGGGCGGCCCATATGATATGCTTATGCA 599

QY 225 AlaLeuSerAspThrValSerArgProValAspIleGlnProPheArgAspMetIle 244

Db 600 GCTTATCCGATACGTGTTCCAAATTTCTGTGCATATTCAGCCATTCAGATATAGTT 659

QY 245 GluGlyMetArgMetAsp 250

Db 660 GAAAGAAATGCGTATGAGC 677

RESULT 14

BM412533

LOCUS

DEFINITION

EST1586860 tomato breaker fruit Lycopersicon esculentum cDNA clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Lycopersicon esculentum (tomato)

Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 634)

Alcala, J., Vrebalov, J., White, R., Vaision, T., Karanycheva, S.A., Tsai, J., Bougri, O., Kirhness, E., Ulteback, T., Van Aken, S., Roming, C.M., Frasier, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.

Generation of ESTs from tomato fruit tissue, breaker stage (2002)

Unpublished

Contact: CUGI

Clemson University Genomics Institute

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>

This clone is available through the Clemson University Genomics Institute

Seq primer: T3.

FEATURES

source Location/Qualifiers

1..634

/organism="Lycopersicon esculentum"

/mol_type="mRNA"

/cultivar="TMA96"

/db_xref="taxon:4081"

/clone="CLEG60114"

/tissue_type="Pericarp"

/dev_stage="breaker"

/lab_host="SOLR"

/clone_lib="tomato breaker fruit"

/note="Vector: pBluescriptSMcadapt, Site 1: EcoRI, Site 2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopen accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

BASE COUNT 200 a 105 c 160 g 169 t

ORIGIN

Alignment Scores:

Pred. No.: 6.58e-105 Length: 634

Score: 997.00 Matches: 194

Percent Similarity: 94.31% Conservative: 5

Best Local Similarity: 91.94% Mismatches: 12

Query Match: 43.92% Indels: 1

DB: 12 Gaps: 0

US-09-847-081b-2 (1-440) x BM412533 (1-634)

QY 155 AlaGluTyrAlaValThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArg 174
 DB 1 GCAGAGATGCAAGACGTTTACTTACCTAGCACTATGCTAAAGACTCCCGAGAGAGAGG 60

QY 175 AlaIleTrrAlaIleTyrValTrrCysArgArgThrAspGluLeuValAspGlyProAsn 194
 DB 61 GCTATTCGGGCAATATGATGTGTGCGAGAGAACAGATGACCTTTGATGCGCCACAC 120

QY 195 AlaSerHisIleThrProGluAlaLeuAspArgTrrGluThrArgLeuGluAspIlePhe 214
 DB 121 GCATCATATATTTACCCCGGACGCTTACATAGTGGGAAATAGGCTAGAGATGTTTTC 180

QY 215 SerGlyArgProPheAspMetLeuAspAlaAlaLeuSerAspThrValSerArgPhePro 234
 DB 181 AATGGGGGGCCATTGACATGCTCGATGCTCTTGTCCGATACAGTTTCTTACTTTCCA 240

QY 235 ValAspIleGlnProPheArgAspMetIleGluGluMetArgMetAspLeuTrrLysSer 254
 DB 241 GTTATATTCACGCAATTCAGATATGATTAAGGAATGCGTATGAGCTTAGAGAAATCG 300

QY 255 ArgTyrIleThrPheAspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGly 274
 DB 301 AGATACAAAACCTTCAGACGACTATACCTTATTGTTATTTGTTGCTGATCGGTTGG 360

QY 275 LeuMetSerValProValMetGlyIleAlaProGluSerLysValThrThrGluSerVal 294
 DB 361 TTGATGAGTGTTCATATATGATGCTATCGCCCTGATCAAGCAACAGAGAGGCGCTA 420

QY 295 TyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGluLeuThrAsnIleLeuArgAspVal 314
 DB 421 TATATGCTGCTTTGGCTCTGGAGATGCGCAATCAATTAACATACATACAGAGATGT 480

QY 315 GlyLysAlaAspAlaArgArgGlyArgValTyrLeuProGluAspGluLeuAlaGly 334
 DB 481 GGAAGAGATGCGCAGAGAGAGAGAGTCTACTTGCCTCAAGTGAATTGACAGGCGAGT 540

QY 335 LeuSerAspGluAspIlePheAlaGlyArgValThrAspLysTrrPheAsnPheMetLys 354
 DB 541 CTATCCGATGAAGATATATTGCTGAGAGGCTGACCGATAATGAGAGATCTTTATGAG 600

QY 355 LysGlnIleGlnArgAlaArgLysPheAsp 365
 DB 601 AACCAATA-CATAGGGGCGAGAAAGTTCTTGAT 632

RESULT 15
 CA999095 704 bp mRNA linear EST 10-JAN-2003
 LOCUS S234N_H03 Rice cold stress germination cDNA library Oryza sativa
 DEFINITION (japonica cultivar-group) cDNA 5', mRNA sequence.
 ACCESSION CA999095
 VERSION CA999095.1 GI:27576401
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzaceae; Oryza.
 1 (bases 1 to 704)
 de los Reyes, B.G., Moray, M., Gibbons, J., Varma, T.S.N., Antoine, W.,
 Redus, M., McGrath, J.M., and Halgren, R.,
 Development of a chilling stress EST library of germinating rice
 (Oryza sativa L. subsp. japonica) enriched with stress-related and
 novel genes
 Unpublished
 JOURNAL Contact: Benildo G. de los Reyes
 COMMENT Plant Genomics Lab., Department of Crop, Soil and Environmental
 Sciences
 University of Arkansas
 115 Plant Science Building, Fayetteville, AR 72701, USA

FEATURES
 source

1. 704
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="P1560247"
 /db_xref="taxon:39947"
 /tissue_type="coleoptile, radicle, prophyll, immature leaf"
 /dev_stage="embryo at different stages of germination and
 shoots of germinated seeds under chilling stress
 (130C/100C)"
 /lab_host="SOLR"
 /clone_lib="rice cold stress germination cDNA library"
 /note="Organ: seedlings; Vector: Lambda Uni-Zap XR excised
 as pBluescript; Site 1: EcoRI; Site 2: XhoI; The cDNAs
 were derived from reverse transcription of mRNA samples
 from seeds at different stages of germination and
 seedlings at early phase of growth under chilling stress
 (130C/100C). The mRNA pool was used as template for double
 stranded cDNA synthesis using the Stratagene Uni-Zap XR
 cDNA synthesis and library kit. A total of 150,000 phages
 were excised from the primary library as pBluescript
 phagemid clones. Enrichment of the primary excised library
 with chilling-induced transcripts was performed by
 hybridizing the primary excised library colony lifts with
 the PCR-select subtraction product, with cold germinated
 cDNA as tester and control temperature-germinated cDNA as
 driver."

BASE COUNT 197 a 150 c 194 g 162 t 1 others

ORIGIN

Alignment Scores:

Pred. No.: 2,48e-103 Length: 704
 Score: 984.00 Matches: 183
 Percent Similarity: 92.48% Conservative: 26
 Best Local Similarity: 80.97% Mismatches: 17
 Query Match: 43.35% Indels: 0
 DB: 14 Gaps: 0

US-09-847-081b-2 (1-440) x CA999095 (1-704)

QY 203 LeuAspArgTrrGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeu 222
 DB 3 CTTCATCGATGCGGAGAGATTAAGAGATCTTTCAGAGCGAGCGCATATGATATGTAT 62

QY 223 AspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArgAsp 242
 DB 63 GATCGACCCCTCTCGGACACAGCTCAAGTTTCCAGTACATTCACGCCATTCAAAGAC 122

QY 243 MetIleGluGlyMetArgMetAspLeuTrrLysSerArgTyrIleThrPheAspGluLeu 262
 DB 123 ATGATTAGAGGAATGAGGCTTGACCTGTGGAATCAAGTATAGAGCTTTGATGAGCTC 182

QY 263 TyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282
 DB 183 TACCTTACATGCTACTACGTTGCTGCGACGCTTGCTTCATGACAGTACCGTATGCGG 242

QY 283 IleAlaProGluSerLysValThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGly 302
 DB 243 ATTCGCCCCGATCGAAGGCTTCAACCGAGACGTATCAACGCTGCGCTTGCTTGGG 302

QY 303 LeuAlaAsnGluLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArg 322
 DB 303 ATCCCAACAGAGCTGAGATATTTCTCAGAGAGCTAGGCGAAGCTCAAGAGGGAAGA 362

QY 323 ValTyrLeuProGluAspGluLeuAlaGlyLeuSerAspGluAspIlePheAla 342
 DB 363 ATCTACCTTCATGATGATGATGAGAGGAGGAGCTGACAGAGAAAGACATATTTGAGA 422

Tel: (479) -575-7465
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 Email: breyes@ark.edu
 Plate: S234N row: H column: 03
 Seq primer: T3.
 Location/Qualifiers

[illegible]

Search completed: January 16, 2004, 08:47:18
Job time : 2829 secs

